

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 3, 2005, 08:08:21 ; Search time 3 Seconds
(without alignments)
481.084 Million cell updates/sec

Title: US-10-616-279-10

Perfect score: 85

Sequence: 1 HSSDYSWVRKNQVVS 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	54.1	438	1 ALBH	alpha-amylase (EC
2	43.5	51.2	545	2 T40207	hypothetical prote
3	42	49.4	435	2 JC7137	alpha-amylase (EC
4	42	49.4	435	2 S12625	alpha-amylase (EC
5	42	49.4	729	2 C84854	ferric-coprogen re
6	42	49.4	729	2 H90813	outer membrane rec
7	42	49.4	729	2 D85673	outer membrane rec
8	42	49.4	877	2 S58824	probable membrane
9	42	49.4	1080	2 A71485	probable pbp2-tran
10	42	49.4	3587	2 T40486	surfactin syntheta
11	41	48.2	121	2 E97103	hypothetical prote
12	41	48.2	304	2 D82189	conserved hypothet
13	41	48.2	372	2 G89921	alanine dehydrogen
14	41	48.2	410	2 S77661	hypothetical prote
15	41	48.2	432	2 G90268	conserved hypothet
16	41	48.2	805	2 T34212	hypothetical prote
17	40	47.1	135	2 C21826	alpha-amylase (EC
18	40	47.1	153	2 A21826	alpha-amylase (EC
19	40	47.1	299	2 D82880	cytosine-specific
20	40	47.1	337	2 AD3614	glycosyl transfera
21	40	47.1	423	2 T09942	alpha-amylase (EC
22	40	47.1	427	1 ALBHB	alpha-amylase (EC
23	40	47.1	429	1 J80406	sensor protein Uhp
24	40	47.1	527	2 A82431	alpha-amylase (EC
25	40	47.1	836	2 T42323	hypothetical prote
26	40	47.1	1179	2 T35093	DNA-directed DNA p
27	39	45.9	88	2 AF1023	hypothetical prote
28	39	45.9	111	2 B25159	13K sin operon hyp
29	39	45.9	279	2 D82243	transcription regu

30	39	45.9	379	2 T50967	probable pyruvate
31	39	45.9	425	2 S68305	gag polyprotein -
32	39	45.9	437	2 JC7138	alpha-amylase (EC
33	39	45.9	440	2 S14958	alpha-amylase (EC
34	39	45.9	446	2 H90063	hypothetical prote
35	39	45.9	494	2 T28660	probable adhesin p
36	39	45.9	568	2 T28876	hypothetical prote
37	39	45.9	1085	2 S55352	IFH1 protein - yea
38	39	45.9	1150	2 T15277	hypothetical prote
39	38	44.7	69	2 FC1257	alpha-amylase (EC
40	38	44.7	260	2 T22990	hypothetical prote
41	38	44.7	261	2 D86729	hypothetical prote
42	38	44.7	296	2 T12770	probable endonucle
43	38	44.7	347	2 T23944	hypothetical prote
44	38	44.7	393	2 S39383	cyclin CCL1 - years
45	38	44.7	415	2 B84544	probable WD-40 rep

ALIGNMENTS

RESULT 1

ALBH

alpha-amylase (EC 3.2.1.1) precursor - barley

C;Species: Hordeum vulgare (barley)

C;Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 09-Jul-2004

C;Accession: A00846; S65602

R;Rogers, J.C.; Millman, C.

J. Biol. Chem. 258, 8169-8174, 1983

A;Title: Isolation and sequence analysis of a barley alpha-amylase cDNA clone.

A;Reference number: A00846; MUID:83238423; PMID:6150808

A;Accession: A00846

A;Molecule type: mRNA

A;Residues: 1-438 <ROG>

A;Cross-references: UNIPROT:P00693; GB:J01236; NID:g166986; PIDN:AAA32929.1; PID:g166987

A;Experimental source: cv. Himalaya

R;Juge, N.; Rodenburg, K.W.; Guo, X.J.; Chaix, J.C.; Svensson, B.

FEBS Lett. 363, 299-303, 1995

A;Title: Isozyme hybrids within the protruding third loop domain of the barley alpha-amylase

A;Reference number: S65602; MUID:95255567; PMID:7737421

A;Accession: S65602

A;Molecule type: protein

A;Residues: 25-29 <JUG>

C;Comment: Production of this enzyme in barley is hormonally regulated. Germinating barle

C;Function:

A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A;Pathway: glycogen/starch degradation

C;Superfamily: wheat alpha-amylase; alpha-amylase core homology

C;Keywords: calcium binding; glycosidase; hydrolase; monomer; polysaccharide degradation

F;1-24/Domain: signal sequence #status predicted <Sig>

F;25-438/Product: alpha-amylase #status predicted <MAT>

F;171-318/Domain: alpha-amylase core homology <AMY>

F;204,229,315/Active site: Asp, Glu, Asp #status experimental

Query Match 54.1%; Score 46; DB 1; Length 438;

Best Local Similarity 54.5%; Pred. No. 9.7;

Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HSSDYSWVRKN 11

Db 419 HGNDYAVWEKN 429

RESULT 2

T40207

hypothetical protein SPBC31F10.04c - fission yeast (Schizosaccharomyces pombe)

C;Species: Schizosaccharomyces pombe

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C;Accession: T40207

R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Pohl, T.

submitted to the EMBL Data Library, August 1997

A;Reference number: T21913

A;Accession: T40207

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-545 <WOO>
A;Cross-references: UNIPROT:P87306; EMBL:Z97204; PIDN:CAB10081.1; GSPDB:GN00067; SPDB:SF
A;Experimental source: strain 972H-; cosmid c31F10
C;Genetics:
A;Gene: SPDB:SPBC31F10.04c
A;Map position: 2
A;Introns: 30/2; 113/2

Query Match 51.2%; Score 43.5; DB 2; Length 545;
Best Local Similarity 56.2%; Pred. No. 30;
Matches 9; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 1 HSSDYSWVR-KNOVVS 15

Db 502 HGTDKSVWRCKDQYSS 517

RESULT 3

JC7137
N;Alternate names: 1,4-gulcan glucanohydrolase I
C;Species: Oryza sativa (rice)
C;Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 11-May-2000
C;Accession: JC7137; PC7039
R;Abe, R.; Yoshida, K.; Aoyagi, M.; Kasahara, S.; Ichishima, E.; Nakajima, T.
BioSci. Biotechnol. Biochem. 63, 1329-1335, 1999
A;Title: Characterization of chimeric enzymes constructed between two distinct alpha-amylase
A;Reference number: JC7137; MUID:99430781; PMID:10500994
A;Accession: JC7137
A;Molecule type: mRNA
A;Residues: 1-435 <ABE>
A;Accession: PC7039
A;Molecule type: protein
A;Residues: 245-252 <AB2>
C;Comment: This enzyme catalyzes the hydrolysis of internal alpha-glucosidic linkages in
is important in germinating seeds and is present as multiple isoforms.
C;Genetics:
A;Gene: amy-I
C;Superfamily: wheat alpha-amylase; alpha-amylase core homology
C;Keywords: calcium binding; germination; glycosidase; hydrolase; seed

Query Match 49.4%; Score 42; DB 2; Length 435;
Best Local Similarity 60.0%; Pred. No. 42;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 HSSDYSWVRK 10

Db 415 HGKDYSVWEK 424

RESULT 4

S12625
alpha-amylase (EC 3.2.1.1) 3D - rice
C;Species: Oryza sativa (rice)
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
C;Accession: S12625; S12776; S15054; JT0945
R;Huang, N.; Koizumi, N.; Reini, S.; Rodriguez, R.L.
Nucleic Acids Res. 19, 7007-7014, 1990
A;Title: Structural organization and differential expression of rice alpha-amylase genes
A;Reference number: JT0945; MUID:91088278; PMID:2263460
A;Accession: S12625
A;Molecule type: DNA
A;Residues: 1-435 <HUA>
A;Cross-references: UNIPROT:P27933; EMBL:M59351; NID:g169770; PIDN:AAA33895.1; PID:g1697
R;O'Neill, S.D.; Kumagai, M.H.; Majumdar, A.; Huang, N.; Sutliff, T.D.; Rodriguez, R.L.
Mol. Gen. Genet. 221, 235-244, 1990
A;Title: The alpha-amylase genes in Oryza sativa: characterization of cDNA clones and mR
A;Reference number: S12775; MUID:90318322; PMID:2370848
A;Accession: S12776
A;Molecule type: mRNA
A;Residues: 1-435 <ONE>

A;Cross-references: EMBL:M24287
R;O'Neill, S.D.; Kumagai, M.H.; Majumdar, A.; Huang, N.; Sutliff, T.D.; Rodriguez, R.L.
submitted to the EMBL Data Library, April 1989
A;Description: The alpha-amylase genes in Oryza sativa: Characterization of cDNA clones &
A;Reference number: S15054
A;Accession: S15054
A;Molecule type: mRNA
A;Residues: 1-72, 'R', 75-136, 'R', 138-435 <ON2>
A;Cross-references: EMBL:M24287; NID:g169754; PIDN:AAA33886.1; PID:g169755
C;Genetics:
A;Introns: 30/3; 342/3
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: wheat alpha-amylase; alpha-amylase core homology
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;170-314/Domain: alpha-amylase core homology <AMY>
F;203,228,311/Active site: Asp, Glu, Asp #status predicted

Query Match 49.4%; Score 42; DB 2; Length 435;
Best Local Similarity 60.0%; Pred. No. 42;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 HSSDYSWVRK 10

Db 415 HGKDYSVWEK 424

RESULT 5

C64854
ferric-coprogen receptor precursor - Escherichia coli (strain K-12)
N;Alternate names: outer membrane protein fhuE
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C;Accession: C64854; S09262; A26875; PC4409
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: C64854
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-729 <BLAT>
A;Cross-references: UNIPROT:P16869; GB:AE000210; GB:U000096; NID:g1787332; PIDN:AAC74186.1
A;Experimental source: strain K-12, substrain MG1655
R;Sauer, M.; Hantke, K.; Braun, V.
Mol. Microbiol. 4, 427-437, 1990
A;Title: Sequence of the fhuE outer-membrane receptor gene of Escherichia coli K12 and p
A;Reference number: S09262; MUID:90286919; PMID:2162465
A;Accession: S09262
A;Molecule type: DNA
A;Residues: 1-362, 'C', 364-729 <SAU>
A;Cross-references: EMBL:X17615; NID:g41448; PIDN:CAA35616.1; PID:g41449
A;Experimental source: strain K-12
R;Sauer, M.; Hantke, K.; Braun, V.
J. Bacteriol. 169, 2044-2049, 1987
A;Title: Ferric-coprogen receptor fhuE of Escherichia coli: processing and sequence comm

A;Accession: A26875

A;Molecule type: DNA

A;Residues: 1-69 <SA2>

R;Kobayashi, Y.; Sasanuma, A.; Nishimura, A.; Kuratomi, K.

Res. Commun. Biochem. Cell Mol. Biol. 1, 157-170, 1997

A;Title: A novel 14-kilodalton protein in P1,P4-bis(5'-adenosyl)tetrathosphate (ap4A)-bir

A;Reference number: JC5685

A;Accession: PC4409

A;Molecule type: DNA

A;Residues: 1-47 <KOB>

C;Genetics:

A;Gene: fhuE

A;Map position: 16 min

C;Function:

A;Description: required for uptake of iron(III) via coprogen, ferrioxamine B and rhodotoxin C;Superfamily: ferrichrome-iron receptor; tonB-dependent receptor amino-terminal homologous C;Keywords: iron transport; membrane protein; receptor
F;1-36/Domain: signal sequence #status predicted <SIG>
F;37-729/Product: outer membrane protein fhue #status predicted <MAT>
F;97-230/Domain: tonB-dependent receptor amino-terminal homologous <TNC>
F;462-729/Domain: tonB-dependent receptor carboxyl-terminal homologous <TNC>

Query Match 49.4%; Score 42; DB 2; Length 729;
Best Local Similarity 42.9%; Pred. No. 70;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 2 SSDYSMRKNQYVS 15
Db 195 SAEYGSWKNERYA 208

RESULT 6
H90813
outer membrane receptor for ferric iron uptake ECs1480 [imported] - Escherichia coli (strain O157:H7)
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: H90813
R;Hayaehi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic maps of the complete genome
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: H90813
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-729 <HAY>
A;Cross-references: UNIPROT:Q8X8H4; GB:BA000007; PIDN:BA034903.1; PID:G13360944; GSPDB:G13360944
A;Experimental source: strain O157:H7, substrain RIMD 050952
C;Genetics:
A;Gene: ECs1480
C;Superfamily: ferric-pseudobactin receptor; tonB-dependent receptor amino-terminal homologous

Query Match 49.4%; Score 42; DB 2; Length 729;
Best Local Similarity 42.9%; Pred. No. 70;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 2 SSDYSMRKNQYVS 15
Db 195 SAEYGSWKNERYA 208

RESULT 7
D85673
outer membrane receptor for ferric iron uptake [imported] - Escherichia coli (strain O157:H7)
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: D85673
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, M.W.; Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, J.; Bowers, J.; Fierman, J.; He, X.; Holt, J.; Karp, P.; Laskin, J.; Laskin, M.; Laskin, N.; Laskin, P.; Laskin, R.; Laskin, S.; Laskin, T.; Laskin, U.; Laskin, V.; Laskin, W.; Laskin, X.; Laskin, Y.; Laskin, Z.; Laskin, AA; Laskin, AB; Laskin, AC; Laskin, AD; Laskin, AE; Laskin, AF; Laskin, AG; Laskin, AH; Laskin, AI; Laskin, AJ; Laskin, AK; Laskin, AL; Laskin, AM; Laskin, AN; Laskin, AO; Laskin, AP; Laskin, AQ; Laskin, AR; Laskin, AS; Laskin, AT; Laskin, AU; Laskin, AV; Laskin, AW; Laskin, AX; Laskin, AY; Laskin, AZ; Laskin, BA; Laskin, BB; Laskin, BC; Laskin, BD; Laskin, BE; Laskin, BF; Laskin, BG; Laskin, BH; Laskin, BI; Laskin, BJ; Laskin, BK; Laskin, BL; Laskin, BM; Laskin, BN; Laskin, BO; Laskin, BP; Laskin, BQ; Laskin, BR; Laskin, BS; Laskin, BT; Laskin, BU; Laskin, BV; Laskin, BW; Laskin, BX; Laskin, BY; Laskin, BZ; Laskin, CA; Laskin, CB; Laskin, CC; Laskin, CD; Laskin, CE; Laskin, CF; Laskin, CG; Laskin, CH; Laskin, CI; Laskin, CJ; Laskin, CK; Laskin, CL; Laskin, CM; Laskin, CN; Laskin, CO; Laskin, CP; Laskin, CQ; Laskin, CR; Laskin, CS; Laskin, CT; Laskin, CU; Laskin, CV; Laskin, CW; Laskin, CX; Laskin, CY; Laskin, CZ; Laskin, DA; Laskin, DB; Laskin, DC; Laskin, DD; Laskin, DE; Laskin, DF; Laskin, DG; Laskin, DH; Laskin, DI; Laskin, DJ; Laskin, DK; Laskin, DL; Laskin, DM; Laskin, DN; Laskin, DO; Laskin, DP; Laskin, DQ; Laskin, DR; Laskin, DS; Laskin, DT; Laskin, DU; Laskin, DV; Laskin, DW; Laskin, DX; Laskin, DY; Laskin, DZ; Laskin, EA; Laskin, EB; Laskin, EC; Laskin, ED; Laskin, EE; Laskin, EF; Laskin, EG; Laskin, EH; Laskin, EI; Laskin, EJ; Laskin, EK; Laskin, EL; Laskin, EM; Laskin, EN; Laskin, EO; Laskin, EP; Laskin, EQ; Laskin, ER; Laskin, ES; Laskin, ET; Laskin, EU; Laskin, EV; Laskin, EW; Laskin, EX; Laskin, EY; Laskin, EZ; Laskin, FA; Laskin, FB; Laskin, FC; Laskin, FD; Laskin, FE; Laskin, FF; Laskin, FG; Laskin, FH; Laskin, FI; Laskin, FJ; Laskin, FK; Laskin, FL; Laskin, FM; Laskin, FN; Laskin, FO; Laskin, FP; Laskin, FQ; Laskin, FR; Laskin, FS; Laskin, FT; Laskin, FU; Laskin, FV; Laskin, FW; Laskin, FX; Laskin, FY; Laskin, FZ; Laskin, GA; Laskin, GB; Laskin, GC; Laskin, GD; Laskin, GE; Laskin, GF; Laskin, GG; Laskin, GH; Laskin, GI; Laskin, GJ; Laskin, GK; Laskin, GL; Laskin, GM; Laskin, GN; Laskin, GO; Laskin, GP; Laskin, GQ; Laskin, GR; Laskin, GS; Laskin, GT; Laskin, GU; Laskin, GV; Laskin, GW; Laskin, GX; Laskin, GY; Laskin, GZ; Laskin, HA; Laskin, HB; Laskin, HC; Laskin, HD; Laskin, HE; Laskin, HF; Laskin, HG; Laskin, HH; Laskin, HI; Laskin, HJ; Laskin, HK; Laskin, HL; Laskin, HM; Laskin, HN; Laskin, HO; Laskin, HP; Laskin, HQ; Laskin, HR; Laskin, HS; Laskin, HT; Laskin, HU; Laskin, HV; Laskin, HW; Laskin, HX; Laskin, HY; Laskin, HZ; Laskin, IA; Laskin, IB; Laskin, IC; Laskin, ID; Laskin, IE; Laskin, IF; Laskin, IG; Laskin, IH; Laskin, II; Laskin, IJ; Laskin, IK; Laskin, IL; Laskin, IM; Laskin, IN; Laskin, IO; Laskin, IP; Laskin, IQ; Laskin, IR; Laskin, IS; Laskin, IT; Laskin, IU; Laskin, IV; Laskin, IW; Laskin, IX; Laskin, IY; Laskin, IZ; Laskin, JA; Laskin, JB; Laskin, JC; Laskin, JD; Laskin, JE; Laskin, JF; Laskin, JG; Laskin, JH; Laskin, JI; Laskin, JJ; Laskin, JK; Laskin, JL; Laskin, JM; Laskin, JN; Laskin, JO; Laskin, JP; Laskin, JQ; Laskin, JR; Laskin, JS; Laskin, JT; Laskin, JU; Laskin, JV; Laskin, JW; Laskin, JX; Laskin, JY; Laskin, JZ; Laskin, KA; Laskin, KB; Laskin, KC; Laskin, KD; Laskin, KE; Laskin, KF; Laskin, KG; Laskin, KH; Laskin, KI; Laskin, KJ; Laskin, KK; Laskin, KL; Laskin, KM; Laskin, KN; Laskin, KO; Laskin, KP; Laskin, KQ; Laskin, KR; Laskin, KS; Laskin, KT; Laskin, KU; Laskin, KV; Laskin, KW; Laskin, KX; Laskin, KY; Laskin, KZ; Laskin, LA; Laskin, LB; Laskin, LC; Laskin, LD; Laskin, LE; Laskin, LF; Laskin, LG; Laskin, LH; Laskin, LI; Laskin, LJ; Laskin, LK; Laskin, LL; Laskin, LM; Laskin, LN; Laskin, LO; Laskin, LP; Laskin, LQ; Laskin, LR; Laskin, LS; Laskin, LT; Laskin, LU; Laskin, LV; Laskin, LW; Laskin, LX; Laskin, LY; Laskin, LZ; Laskin, MA; Laskin, MB; Laskin, MC; Laskin, MD; Laskin, ME; Laskin, MF; Laskin, MG; Laskin, MH; Laskin, MI; Laskin, MJ; Laskin, MK; Laskin, ML; Laskin, MN; Laskin, MO; Laskin, MP; Laskin, MQ; Laskin, MR; Laskin, MS; Laskin, MT; Laskin, MU; Laskin, MV; Laskin, MW; Laskin, MX; Laskin, MY; Laskin, MZ; Laskin, NA; Laskin, NB; Laskin, NC; Laskin, ND; Laskin, NE; Laskin, NF; Laskin, NG; Laskin, NH; Laskin, NI; Laskin, NJ; Laskin, NK; Laskin, NL; Laskin, NM; Laskin, NO; Laskin, NP; Laskin, NQ; Laskin, NR; Laskin, NS; Laskin, NT; Laskin, NU; Laskin, NV; Laskin, NW; Laskin, NX; Laskin, NY; Laskin, NZ; Laskin, OA; Laskin, OB; Laskin, OC; Laskin, OD; Laskin, OE; Laskin, OF; Laskin, OG; Laskin, OH; Laskin, OI; Laskin, OJ; Laskin, OK; Laskin, OL; Laskin, OM; Laskin, ON; Laskin, OO; Laskin, OP; Laskin, OQ; Laskin, OR; Laskin, OS; Laskin, OT; Laskin, OU; Laskin, OV; Laskin, OW; Laskin, OX; Laskin, OY; Laskin, OZ; Laskin, PA; Laskin, PB; Laskin, PC; Laskin, PD; Laskin, PE; Laskin, PF; Laskin, PG; Laskin, PH; Laskin, PI; Laskin, PJ; Laskin, PK; Laskin, PL; Laskin, PM; Laskin, PN; Laskin, PO; Laskin, PP; Laskin, PQ; Laskin, PR; Laskin, PS; Laskin, PT; Laskin, PU; Laskin, PV; Laskin, PW; Laskin, PX; Laskin, PY; Laskin, PZ; Laskin, QA; Laskin, QB; Laskin, QC; Laskin, QD; Laskin, QE; Laskin, QF; Laskin, QG; Laskin, QH; Laskin, QI; Laskin, QJ; Laskin, QK; Laskin, QL; Laskin, QM; Laskin, QN; Laskin, QO; Laskin, QP; Laskin, QQ; Laskin, QR; Laskin, QS; Laskin, QT; Laskin, QU; Laskin, QV; Laskin, QW; Laskin, QX; Laskin, QY; Laskin, QZ; Laskin, RA; Laskin, RB; Laskin, RC; Laskin, RD; Laskin, RE; Laskin, RF; Laskin, RG; Laskin, RH; Laskin, RI; Laskin, RJ; Laskin, RK; Laskin, RL; Laskin, RM; Laskin, RN; Laskin, RO; Laskin, RP; Laskin, RQ; Laskin, RR; Laskin, RS; Laskin, RT; Laskin, RU; Laskin, RV; Laskin, RW; Laskin, RX; Laskin, RY; Laskin, RZ; Laskin, SA; Laskin, SB; Laskin, SC; Laskin, SD; Laskin, SE; Laskin, SF; Laskin, SG; Laskin, SH; Laskin, SI; Laskin, SJ; Laskin, SK; Laskin, SL; Laskin, SM; Laskin, SN; Laskin, SO; Laskin, SP; Laskin, SQ; Laskin, SR; Laskin, SS; Laskin, ST; Laskin, SU; Laskin, SV; Laskin, SW; Laskin, SX; Laskin, SY; Laskin, SZ; Laskin, TA; Laskin, TB; Laskin, TC; Laskin, TD; Laskin, TE; Laskin, TF; Laskin, TG; Laskin, TH; Laskin, TI; Laskin, TJ; Laskin, TK; Laskin, TL; Laskin, TM; Laskin, TN; Laskin, TO; Laskin, TP; Laskin, TQ; Laskin, TR; Laskin, TS; Laskin, TT; Laskin, TU; Laskin, TV; Laskin, TW; Laskin, TX; Laskin, TY; Laskin, TZ; Laskin, UA; Laskin, UB; Laskin, UC; Laskin, UD; Laskin, UE; Laskin, UF; Laskin, UG; Laskin, UH; Laskin, UI; Laskin, UJ; Laskin, UK; Laskin, UL; Laskin, UM; Laskin, UN; Laskin, UO; Laskin, UP; Laskin, UQ; Laskin, UR; Laskin, US; Laskin, UT; Laskin, UU; Laskin, UV; Laskin, UW; Laskin, UX; Laskin, UY; Laskin, UZ; Laskin, VA; Laskin, VB; Laskin, VC; Laskin, VD; Laskin, VE; Laskin, VF; Laskin, VG; Laskin, VH; Laskin, VI; Laskin, VJ; Laskin, VK; Laskin, VL; Laskin, VM; Laskin, VN; Laskin, VO; Laskin, VP; Laskin, VQ; Laskin, VR; Laskin, VS; Laskin, VT; Laskin, VU; Laskin, VV; Laskin, VW; Laskin, VX; Laskin, VY; Laskin, VZ; Laskin, WA; Laskin, WB; Laskin, WC; Laskin, WD; Laskin, WE; Laskin, WF; Laskin, WG; Laskin, WH; Laskin, WI; Laskin, WJ; Laskin, WK; Laskin, WL; Laskin, WM; Laskin, WN; Laskin, WO; Laskin, WP; Laskin, WQ; Laskin, WR; Laskin, WS; Laskin, WT; Laskin, WU; Laskin, WV; Laskin, WW; Laskin, WX; Laskin, WY; Laskin, WZ; Laskin, XA; Laskin, XB; Laskin, XC; Laskin, XD; Laskin, XE; Laskin, XF; Laskin, XG; Laskin, XH; Laskin, XI; Laskin, XJ; Laskin, XK; Laskin, XL; Laskin, XM; Laskin, XN; Laskin, XO; Laskin, XP; Laskin, XQ; Laskin, XR; Laskin, XS; Laskin, XT; Laskin, XU; Laskin, XV; Laskin, XW; Laskin, XX; Laskin, XY; Laskin, XZ; Laskin, YA; Laskin, YB; Laskin, YC; Laskin, YD; Laskin, YE; Laskin, YF; Laskin, YG; Laskin, YH; Laskin, YI; Laskin, YJ; Laskin, YK; Laskin, YL; Laskin, YM; Laskin, YN; Laskin, YO; Laskin, YP; Laskin, YQ; Laskin, YR; Laskin, YS; Laskin, YT; Laskin, YU; Laskin, YV; Laskin, YW; Laskin, YX; Laskin, YY; Laskin, YZ; Laskin, ZA; Laskin, ZB; Laskin, ZC; Laskin, ZD; Laskin, ZE; Laskin, ZF; Laskin, ZG; Laskin, ZH; Laskin, ZI; Laskin, ZJ; Laskin, ZK; Laskin, ZL; Laskin, ZM; Laskin, ZN; Laskin, ZO; Laskin, ZP; Laskin, ZQ; Laskin, ZR; Laskin, ZS; Laskin, ZT; Laskin, ZU; Laskin, ZV; Laskin, ZW; Laskin, ZX; Laskin, ZY; Laskin, ZZ

Db 195 SAEYGSWKNERYA 208

RESULT 8
S58824
Probable membrane protein YPR194c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein P9677.13
C;Species: Saccharomyces cerevisiae
C;Date: 28-Nov-1995 #sequence_revision 19-Jan-1996 #text_change 09-Jul-2004
C;Accession: S58824
R;Miller, N.
submitted to the EMBL Data Library, April 1995
A;Description: The sequence of S. cerevisiae cosmid 9677.
A;Reference number: S58816
A;Accession: S58824
A;Molecule type: DNA
A;Residues: 1-877 <MIL>
A;Cross-references: UNIPROT:Q06593; EMBL:U25841; NID:g786295; PID:g786296; GSPDB:GN00016;
C;Genetics:
A;Gene: SGD:OPT2; MIPS:YPR194C
A;Cross-references: SGD:S0006398
A;Map position: 16R
C;Superfamily: Saccharomyces cerevisiae probable membrane protein YJL212c
C;Keywords: transmembrane protein
F;278-294/Domain: transmembrane #status predicted <TM1>
F;409-425/Domain: transmembrane #status predicted <TM2>
F;485-501/Domain: transmembrane #status predicted <TM3>
F;558-574/Domain: transmembrane #status predicted <TM4>
F;586-602/Domain: transmembrane #status predicted <TM5>
F;689-685/Domain: transmembrane #status predicted <TM6>
F;734-750/Domain: transmembrane #status predicted <TM7>
F;816-832/Domain: transmembrane #status predicted <TM8>

Query Match 49.4%; Score 42; DB 2; Length 877;
Best Local Similarity 42.9%; Pred. No. 84;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 HSDYSMRKNQYV 14
Db 36 HSDFSQWYTDQI 49

RESULT 9
A71485
probable pbp2-transglycolase/transpeptidase - Chlamydia trachomatis (serotype D, strain 1
C;Species: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
C;Accession: A71485
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tract
A;Reference number: A71570; MUID:99000809; PMID:9784136
A;Accession: A71485
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1080 <ARN>
A;Cross-references: UNIPROT:O84688; GB:AE001338; NID:g3329126; PIDN:AAC6827;
A;Experimental source: serotype D, strain UW-3/Cx
C;Genetics:
A;Gene: pbpB

Query Match 49.4%; Score 42; DB 2; Length 1080;
Best Local Similarity 54.5%; Pred. No. 1e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 4 DYSMRKNQYV 14
Db 330 DYQWROQQYL 340

RESULT 10
140486

surfactin synthetase component II - Bacillus subtilis
 N;Alternate names: surfactin synthetase srfA2; surfactin synthetase/competence protein s
 N;Contents: acid-amino-acid ligase (EC 6.3.2.-)
 C;Species: Bacillus subtilis
 C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
 C;Accession: 140486; S60866; C69718; S46968; S35518; S25658; S34986
 R;Cosmina, P.; Rodriguez, F.; de Ferra, F.; Grandi, G.; Perego, M.; Venema, G.; van Sind
 Mol. Microbiol. 8, 821-831, 1993
 A;Title: Sequence and analysis of the genetic locus responsible for surfactin synthesis
 A;Reference number: 140485; MUID:93360813; PMID:8355609
 A;Accession: 140486
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-3587 <RES>
 A;Cross-references: UNIPROT:Q04747; EMBL:X70356; NID:g396480; PIDN:CAA49817.1; PID:g3964
 A;Experimental source: strain W168 derivative of JH642
 R;Hamons, L.W.; Eshuis, H.; Jongbloed, J.; Venema, G.; van Sinderen, D.
 Mol. Microbiol. 15, 55-63, 1995
 A;Title: A small gene, designated comS, located within the coding region of the fourth a
 A;Reference number: S60866; MUID:95272393; PMID:7752896
 A;Accession: S60866
 A;Molecule type: DNA
 A;Residues: 977-1104 <HAM>
 R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
 C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
 A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
 Nature 390, 249-256, 1997
 A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallen
 Koch, J.; Harwood, C.R.; Henauf, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulio, M.F.
 Koetter, P.; Koningsberg, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
 A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue
 Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
 A;Authors: Schleich, S.; Schroeter, R.; Scroffone, P.; Sekiguchi, J.; Sekowska, A.; Seron
 akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
 A;Authors: Yoshikawa, H.F.; Zumstede, E.; Yoshikawa, H.; Danchin, A.
 A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
 A;Reference number: A69580; MUID:98044033; PMID:9384377
 A;Accession: C69718
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-3587 <KUN>
 A;Cross-references: GB:Z99105; GB:AL009126; NID:g2632457; PIDN:CAB12143.1; PID:g2632635
 A;Experimental source: strain 168
 R;Fabrit, C.; Quantin, Y.; Guiseppi, A.; Busuttil, J.; Haiech, J.; Denizot, F.
 Submitted to the EMBL Data Library, March 1993
 A;Reference number: S46967
 A;Accession: S46968
 A;Molecule type: DNA
 A;Residues: 1-32, 'F', 34-41, 'G', 43-109, 'D', 111-114, 'G', 116-138, 'V', 140-258, 'W', 260-308, 'A
 1756-1914, 'PK', 1917-2138, 'SRL', 2142, 'DSL', 2146-2444, 'Q', 2446-2712, 'H', 2714-2722, 'H', 272
 A;Cross-references: EMBL:X72672; NID:9516358; PIDN:CAA51223.1; PID:9516360
 R;Fuma, S.; Fujishima, Y.; Corbelli, N.; D'Souza, C.; Nakano, M.M.; Zuber, P.; Yamane, K.
 Nucleic Acids Res. 21, 93-97, 1993
 A;Title: Nucleotide sequence of 5' portion of srfA that contains the region required for
 A;Reference number: S35517; MUID:93181186; PMID:8441623
 A;Accession: S35518
 A;Status: significant sequence differences
 A;Molecule type: DNA
 A;Cross-references: EMBL:D13262; NID:g216345; PID:g216347
 A;Experimental source: strain 168 trpC2
 R;Borchert, S.; Patil, S.S.; Marabel, M.A.
 FEMS Microbiol. Lett. 92, 175-180, 1992
 A;Title: Identification of putative multifunctional peptide synthetase genes using high
 A;Reference number: S25658
 A;Accession: S25658
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 168, 'C', 170-171, 281-283; 514-595, 597-647, 'B', 649-679, 'ETL', 683-693, 'DKR', 697,
 A;Cross-references: EMBL:X65835; NID:940202; PIDN:CAA46678.1; PID:940203
 A;Experimental source: strain ATCC 21332
 C;Comment: This protein contains several amino acid-activating domains for the synthesis

the amino-terminal region of this protein, appear to be required for the development of s
 C;Genetics:
 A;Gene: srfAB; srfA2
 C;Superfamily: surfactin synthetase; acetate-CoA ligase homology; acyl carrier protein ho
 C;Keywords: antibiotic biosynthesis; carrier protein; duplication; ligase; phosphopantet
 F;511-951/Domain: acetate-CoA ligase homology <ACLI>
 F;968-1035/Domain: acyl carrier protein homology <ACPI>
 F;1036-1481/Domain: repeat <RPT1>
 F;1542-1995/Domain: acetate-CoA ligase homology <ACL2>
 F;2013-2081/Domain: acyl carrier protein homology <ACP2>
 F;2082-2529/Domain: repeat <RPT2>
 F;2591-3024/Domain: acetate-CoA ligase homology <ACL3>
 F;3041-3108/Domain: acyl carrier protein homology <ACP3>
 F;999,2045,3073/Binding site: phosphopantetheine (Ser) (covalent) #status predicted
 Query Match 49.4%; Score 42; DB 2; Length 3587;
 Best Local Similarity 50.0%; Pred. No. 3.4e+02;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 1 HSSDYSNWRKNQ 12
 Db 1213 HYKDYAVWHKEQ 1224
 RESULT 11
 E971103
 C;Species: Clostridium acetobutylicum
 C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
 C;Accession: E97103
 R;Nolling, J.; Bretton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
 J.; Dally, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
 J. Bacteriol. 183, 4823-4838, 2001
 A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
 A;Reference number: A96900; MUID:21359325; PMID:21359325
 A;Accession: E97103
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-121 <KUR>
 A;Cross-references: UNIPROT:Q971J1; GB:AE001437; PIDN:AAK79616.1; PID:gl5024609; GSPDB:CN
 A;Experimental source: Clostridium acetobutylicum ATCC824
 C;Genetics:
 A;Gene: CAC1650
 Query Match 48.2%; Score 41; DB 2; Length 121;
 Best Local Similarity 58.3%; Pred. No. 17;
 Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 4 DYSMWRKNQYVS 15
 Db 19 DIITWEKNEYS 30
 RESULT 12
 D82189
 C;Species: Vibrio cholerae
 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 C;Accession: D82189
 R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
 chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.
 1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
 A;Reference number: A82035; MUID:20406833; PMID:10952301
 A;Accession: D82189
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-304 <HEI>
 A;Cross-references: UNIPROT:Q9KRV0; GB:AE004231; GB:AE003852; NID:g9656027; PIDN:AAF9468
 A;Experimental source: serogroup O1; strain N16961; biotype El Tor
 C;Genetics:
 A;Gene: VC1534

A:Map position: 1

Query Match 48.2%; Score 41; DB 2; Length 304;
Best Local Similarity 72.7%; Pred. No. 42;
Matches 8; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

Qy 1 HSSDYSWVRKN 11
| | | | |
Db 8 HGSDY--WRKN 16

RESULT 13

G89921
alanine dehydrogenase [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: G89921
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: G89921
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-372 <KUR>
A;Cross-references: UNIPROT:Q90U49; GB:BA000018; PID:g13701237; PIDN:BA842532.1; GSPDB:G
A;Experimental source: strain N315
C:Genetics:
A;Gene: SA1272
C;Superfamily: alanine dehydrogenase; alanine dehydrogenase homology

Query Match 48.2%; Score 41; DB 2; Length 372;
Best Local Similarity 42.9%; Pred. No. 52;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 HSSDYSWVRKNQYV 14
| | | | | : | | : | | :
Db 76 HESEYQYFKKNQII 89

RESULT 14

S77661
hypothetical protein o410 - Mycobacterium leprae
C:Species: Mycobacterium leprae
C;Date: 11-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
C;Accession: S77661; S49524
R;Psithi, H.; Cole, S. T.
Mol. Microbiol. 16, 909-919, 1995
A;Title: The Mycobacterium leprae genome: systematic sequence analysis identifies key ca
A;Reference number: S77652; MUID:96059637; PMID:7476189
A;Accession: S77661
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-410 <FSI>
A;Cross-references: UNIPROT:Q50178; EMBL:246257; NID:g559905; PIDN:CAA86366.1; PID:g5599
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1994

Query Match 48.2%; Score 41; DB 2; Length 410;
Best Local Similarity 46.7%; Pred. No. 57;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 HSSDYSWVRKNQYVS 15
| | | | | : | | : | | :
Db 313 HSSDPNLWHRKFHAS 327

RESULT 15

G90268
conserved hypothetical protein [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004

C;Accession: G90268
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-y
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: G90268
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-432 <KUR>
A;Cross-references: UNIPROT:Q97YZ4; GB:AR006641; NID:gl3814346; PIDN:AAK41406.1; GSPDB:G
C:Genetics:
A;Gene: SS01155

Query Match 48.2%; Score 41; DB 2; Length 432;
Best Local Similarity 54.5%; Pred. No. 60;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 4 DYSWVRKNQYV 14
| | | | | : | | : | | :
Db 12 DWNFWYKNQYV 22

Search completed: June 3, 2005, 08:29:33
Job time : 5 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 3, 2005, 07:50:56 ; Search time 14.1 Seconds
(without alignments)
544.765 Million cell updates/sec

Title: US-10-616-279-10

Perfect score: 85

Sequence: 1 HSSDYSWVRKQVVS 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	100.0	331	1 SPO2 HUMAN	Q8ud66 homo sapien
2	82	96.5	289	2 Q6KA56	Q8ka56 mus musculu
3	82	96.5	330	1 SPO2 MOUSE	Q8bme2 mus musculu
4	82	96.5	330	1 SPO2 RAT	Q8wv75 rattus norv
5	82	96.5	330	2 Q8VD28	Q8vd28 mus musculu
6	63	74.1	331	2 Q42112	Q42112 brachydanio
7	55	64.7	313	2 Q6DCM4	Q6dcM4 xenopus lae
8	49	57.6	138	2 Q82UD3	Q82ud3 nitrosomona
9	49	57.6	420	2 Q22019	Q22019 cyanidiosch
10	49	57.6	446	2 Q85G84	Q85g84 cyanidiosch
11	47	55.3	390	2 Q7Y4U7	Q7y4u7 bacterioph
12	46	54.1	438	1 AMY1 HORVU	P00693 hordeum vul
13	46	54.1	438	2 Q40017	Q40017 hordeum vul
14	46	54.1	1453	2 Q755D1	Q755d1 ashbya goss
15	45	52.9	845	2 Q9GR11	Q9gr11 leishmania
16	44	51.8	434	2 Q81699	Q81699 avena fatua
17	44	51.8	434	2 Q87CW9	Q87cw9 xylella fas
18	44	51.8	437	2 Q81700	Q81700 avena fatua
19	44	51.8	839	2 Q8ML26	Q8ml26 drosophila
20	44	51.8	3099	2 Q7R514	Q7r514 giardia lam
21	43.5	51.2	545	1 SRB4 SCHPO	P87306 schizosacch
22	43.5	51.2	570	2 Q8D4R4	Q8d4r4 vibrio vuln
23	43.5	51.2	602	2 Q7MG88	Q7mg88 vibrio vuln
24	43	50.6	273	1 HIS6 METAC	Q8tt96 methanosarc
25	43	50.6	463	2 Q89KW8	Q89kw8 bradyrhizob
26	43	50.6	809	2 Q7NAP2	Q7naf2 mycoplasma
27	42	49.4	92	2 Q6DC15	Q6dc15 brachydanio
28	42	49.4	105	2 Q73915	Q73915 bacillus ce
29	42	49.4	206	2 Q99L35	Q99l35 mus musculu
30	42	49.4	230	2 Q7T5M1	Q7t5m1 cryptocophle
31	42	49.4	239	2 Q8JR20	Q8jr20 phthorimaea

32	42	49.4	294	1 TNE7 HUMAN	O98588 homo sapien
33	42	49.4	294	2 Q6UW79	O6uw79 homo sapien
34	42	49.4	422	2 Q6YOR6	Q6yqr6 onion yello
35	42	49.4	435	1 AM3D ORYSA	P27933 oryza sativ
36	42	49.4	436	2 Q6ZDD5	Q6zdd5 oryza sativ
37	42	49.4	442	2 Q7SDN5	Q7sdn5 neurospora
38	42	49.4	504	2 Q6L0Z8	Q6l0z8 picophilus
39	42	49.4	729	1 FHUE ECOLI	P16869 escherichia
40	42	49.4	729	2 Q8AF82	Q8af82 escherichia
41	42	49.4	729	2 Q8X8H4	Q8x8h4 escherichia
42	42	49.4	729	2 Q8CW53	Q8cw53 escherichia
43	42	49.4	734	2 Q69DL2	Q69dl2 sus scrofa
44	42	49.4	877	2 Q06593	Q06593 saccharomyc
45	42	49.4	1080	2 O84688	O84688 chlamydia t

ALIGNMENTS

RESULT 1
ID SPO2 HUMAN STANDARD; PRT; 331 AA.
AC Q8UD6; Q9ULW1;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Spondin 2 precursor (Mindin) (Differentially expressed in cancerous
DE and noncancerous lung cells 1) (DIL-1) (UNQ435/PRO866).
GN Name=SPON2; Synonyms=DIL1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN VAL-242.
RP SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND VARIANTS ALA-122 AND
RX MEDLINE=99443867; PubMed=10512675; DOI=10.1006/geno.1999.5939;
RA Manda K., Kohno T., Matsuno Y., Takenoshita S., Kuwano H., Yokota J.;
RT "Identification of genes (SPON2 and C20orf2) differentially expressed
RT between cancerous and noncancerous lung cells by mRNA differential
RT display.";
RL Genomics 61:5-14(1999).
[2]
RN SEQUENCE FROM N.A.
RP MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P., Gray A.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
[3]
RN SEQUENCE FROM N.A. AND VARIANTS ALA-122 AND VAL-242.
RP PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoaka S., Chiba Y.,
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,
RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,

RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
RA Inose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamagaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Komatsu T.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Nakagawa K.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Yamaguchi R.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isoqai T., Sugano S.,
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs.";
RL Nat. Genet. 36:40-45(2004).
RN [4]
RN SEQUENCE FROM N.A.
RC TISSUE=Colon, and Placenta;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
CC -1- FUNCTION: Cell adhesion protein that promote adhesion and
CC outgrowth of hippocampal embryonic neurons. Binds directly to
CC bacteria and their components and functions as an opsonin for
CC macrophage phagocytosis of bacteria. Essential in the initiation
CC of the innate immune response and represents a unique pattern-
CC recognition molecule in the ECM for microbial pathogens (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Secreted. Extracellular matrix (By
CC similarity).
CC -1- TISSUE SPECIFICITY: Expressed in normal lung tissues but not in
CC lung carcinoma cell lines.
CC -1- SIMILARITY: Contains 1 spondin domain.
CC -1- SIMILARITY: Contains 1 TSP type-1 domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC ENBL; AB027466; BA85892.1; -
CC ENBL; AY358948; AA089307.1; -
CC ENBL; AK074618; BAC11092.1; -
CC ENBL; AK074770; BAC11196.1; -
CC ENBL; BC002707; AA02707.1; -
CC ENBL; BC036341; AA036341.1; -
CC Genew; HGNC:11253; SPON2.
CC H-InvDB; HIX0004013; -.

DR MTM; 605918; -.
DR InterPro; IPR009465; Spond_N.
DR InterPro; IPR000884; TSP1.
DR Pfam; PF06468; Spond_N; 1.
DR Pfam; PF00090; TSP_1; 1.
DR PROSITE; PSS1020; SPONDIN; 1.
DR PROSITE; PSS0092; TSP1; 1.
KW Cell adhesion; Extracellular matrix; Immune response; Polymorphism;
KW Signal.
FT SIGNAL 1 26 Potential.
FT CHAIN 27 331 Spondin 2.
FT DOMAIN 31 221 Spondin.
FT DOMAIN 277 331 TSP type-1.
FT VARIANT 40 40 P -> L (in dbSNP:922697).
FT VARIANT 122 122 E -> A (in dbSNP:11247975).
FT VARIANT 242 242 L -> V (in dbSNP:2279279).
FT VARIANT 331 331 /FTID=VAR_019703.
SQ SEQUENCE 331 AA; 35844 MW; 418E244B893C59F4 CRC64;
Query Match 100.0%; Score 85; DB 1; Length 331;
Best Local Similarity 100.0%; Pred. No. 1.2e-05; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HSSDYSMWKKNQYVS 15
DB 77 HSSDYSMWKKNQYVS 91
|||||
RESULT 2
Q6KAS6 PRELIMINARY; PRT; 289 AA.
ID Q6KAS6 PRELIMINARY; PRT; 289 AA.
AC Q6KAS6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MFLJ00108 protein (Fragment).
GN Name=MFLJ00108;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA Saga Y., Kitamura H., Nakagawa T., Nagase T., Ohara O., Koga H.,
RT "Prediction of the Coding Sequences of Mouse Homologues of FLJ Genes:
RT The Complete Nucleotide Sequences of 110 Mouse FLJ-Homologous cDNAs
RT Identified by Screening of Terminal Sequences of cDNA Clones Randomly
RT Sampled from Size-Fractionated Libraries.";
RL DNA Res. 11:167-180(2004).
DR ENBL; AK131131; BAD21381.1; -
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR009465; Spond_N.
DR InterPro; IPR000884; TSP1.
DR Pfam; PF06468; Spond_N; 1.
DR Pfam; PF00090; TSP_1; 1.
DR SMART; SM00209; TSP1; 1.
DR PROSITE; PSS0092; TSP1; 1.
FT NON TER 1 1
SQ SEQUENCE 289 AA; 31664 MW; 7FCE9444C03021E9 CRC64;
Query Match 96.5%; Score 82; DB 2; Length 289;
Best Local Similarity 93.3%; Pred. No. 3.3e-05; Indels 0; Gaps 0;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 HSSDYSMWKKNQYVS 15
DB 35 HSSDYSMWKKNQYVS 49
|||||
RESULT 3

SPO2_MOUSE
ID SPO2_MOUSE STANDARD; PRT; 330 AA.
AC QBMS2; Q6JDB8;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DE 25-JAN-2005 (Rel. 46, Last annotation update)
DE Spondin 2 precursor (Mindin).
GN Name=Spon2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND FUNCTION.
RC TISSUE=Thymus;
RX PubMed=14691481; DOI=10.1038/nr1021;
RA He Y.-W., Li H., Zhang J., Hsu C.-L., Lin E., Zhang N., Guo J.,
RA Forbush K.A., Bevan M.J.;
RT "The extracellular matrix protein mindin is a pattern-recognition
RT molecule for microbial pathogens.";
RL Nat. Immunol. 5:88-97(2004).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaado I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Haegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Maceuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chochia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher K.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sample C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tonita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yangisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Haehizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL Nature 420:563-573(2002).
CC -1- FUNCTION: Cell adhesion protein that promote adhesion and
CC outgrowth of hippocampal embryonic neurons. Binds directly to
CC bacteria and their components and functions as an opsonin for
CC macrophage phagocytosis of bacteria. Essential in the initiation
CC of the innate immune response and represents a unique pattern-
CC recognition molecule in the ECM for microbial pathogens.
CC -1- SUBCELLULAR LOCATION: Secreted. Extracellular matrix.
CC -1- SIMILARITY: Contains 1 spondin domain.
CC -1- SIMILARITY: Contains 1 TSP type-1 domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC EMBL; AK028987; BAC26226.1; -

DR EMBL; AY457639; AAR20834.1; -
DR MGD; MGI:1923724; Spon2.
DR InterPro; IPR009465; Spond N.
DR InterPro; IPR000884; TSP1.
DR Pfam; PF06468; Spond N; 1.
DR Pfam; PF00090; TSP 1; 1.
DR SMART; SM00209; TSP1; 1.
DR PROSITE; PS1020; SPONDIN; 1.
DR PROSITE; PS00092; TSP1; 1.
KW Cell adhesion; Extracellular matrix; Immune response; Signal.
FT SIGNAL 1 25 Potential.
FT CHAIN 26 330 Spondin 2.
FT DOMAIN 30 220 Spondin.
FT DOMAIN 276 330 TSP type-1.
FT CONFLICT 242 242 R -> Q (in Ref. 2).
SQ SEQUENCE 330 AA; 35964 MW; 581F16GA55F9A07 CRC64;
Query Match 96.5%; Score 82; DB 1; Length 330;
Best Local Similarity 93.3%; Pred. No. 3.8e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 HSSDYSNWRKNQYVS 15
DB 76 HSSDYSNWRKNQYVS 90
|||||
RESULT 4
SPO2_RAT
ID SPO2_RAT STANDARD; PRT; 330 AA.
AC Q9WV75;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Spondin 2 precursor (Mindin).
GN Name=Spon2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RN SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=99339921; PubMed=10409509;
RA Feinstein Y., Borrell V., Garcia C., Burszyn-Cohen T., Tzarfaty V.,
RA Frumkin A., Nose A., Okamoto H., Higashijima S., Soriano A., Klar A.;
RA "F-spondin and mindin: two structurally and functionally related genes
RA expressed in the hippocampus that promote outgrowth of embryonic
RA hippocampal neurons.";
RL Development 126:3637-3648(1999).
RN [2]
RN SEQUENCE FROM N.A.
RC TISSUE=Lung;
RG NIH - Mammalian Gene Collection (MGC) project;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Cell adhesion protein that promote adhesion and
CC outgrowth of hippocampal embryonic neurons. Binds directly to
CC bacteria and their components and functions as an opsonin for
CC macrophage phagocytosis of bacteria. Essential in the initiation
CC of the innate immune response and represents a unique pattern-
CC recognition molecule in the ECM for microbial pathogens (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Secreted. Extracellular matrix.
CC -1- TISSUE SPECIFICITY: Abundantly expressed in the developing
CC hippocampus.
CC -1- SIMILARITY: Contains 1 spondin domain.
CC -1- SIMILARITY: Contains 1 TSP type-1 domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC EMBL; AK028987; BAC26226.1; -

CC or send an email to license@isb-sib.ch).

CC -----
DR EMBL; AF15196; AAD38195.1; -;
DR EMBL; BC078734; AAH78734.1; -;
DR RGD; 708584; LOC171569.
DR InterPro; IPR009465; Spond_N.
DR InterPro; IPR00884; TSP1.
DR Pfam; PF06468; Spond_N; 1.
DR Pfam; PF00090; TSP 1; 1.
DR SMART; SM00209; TSP1; 1.
DR PROSITE; PSS1020; SPONDIN; 1.
DR PROSITE; PS50092; TSP1; 1.
KW Cell adhesion; Extracellular matrix; Immune response; Signal.
FT SIGNAL 1 25 Potential.
FT CHAIN 26 330 Spondin 2.
FT DOMAIN 30 220 Spondin.
FT DOMAIN 276 330 TSP type-1.
SQ SEQUENCE 330 AA; 36014 MW; ECBCF07A0345A83A CRC64;

Query Match 96.5%; Score 82; DB 1; Length 330;
Best Local Similarity 93.3%; Pred. No. 3.8e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSSDYSWMRKQYVS 15
Db 76 HSSDYSWMRKQYVS 90
|||||:|||||

RESULT 5

Q8VD28 PRELIMINARY; PRT; 330 AA.
ID Q8VD28
AC Q8VD28;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Spondin 2, extracellular matrix protein.
GN Name=Spond2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnrerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]

SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC017616; AAH17616.1; -;
DR MGD; MG1:1923724; Spond.
DR GO; GO:0005615; C:extracellular space; TAS.

DR Pfam; PF06468; Spond_N; 1.
DR Pfam; PF00090; TSP 1; 1.
DR SMART; SM00209; TSP1; 1.
DR PROSITE; PS50092; TSP1; 1.
KW Matrix protein.
SQ SEQUENCE 330 AA; 35987 MW; FA2B56A257211E37 CRC64;

Query Match 96.5%; Score 82; DB 2; Length 330;
Best Local Similarity 93.3%; Pred. No. 3.8e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSSDYSWMRKQYVS 15
Db 76 HSSDYSWMRKQYVS 90
|||||:|||||

RESULT 6

O42112 PRELIMINARY; PRT; 331 AA.
ID O42112
AC O42112;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MINDIN2.
GN Name=spond2b;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]

SEQUENCE FROM N.A.
RP MEDLINE=98104230; PubMed=9441663; DOI=10.1006/dbio.1997.8760;
RX Higashijima S., Nose A., Eguchi G., Hotta Y., Okamoto H.;
RT "Mindin/F-spondin family: novel ECM proteins expressed in the
RT zebrafish embryonic axis";
RL Dev. Biol. 192:211-227 (1997).
DR EMBL; AB006085; BAA22809.1; -;
DR ZFIN; ZDB-GENE-990415-161; spond2b.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR009465; Spond_N.
DR InterPro; IPR00884; TSP1.
DR Pfam; PF06468; Spond_N; 1.
DR Pfam; PF00090; TSP 1; 1.
DR SMART; SM00209; TSP1; 1.
DR PROSITE; PS50092; TSP1; 1.
SQ SEQUENCE 331 AA; 36887 MW; 1D95D82B6549D273 CRC64;

Query Match 74.1%; Score 63; DB 2; Length 331;
Best Local Similarity 60.0%; Pred. No. 0.049;
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HSSDYSWMRKQYVS 15
Db 76 HSSDYSWMRKQYVS 90
|||||:|||||

RESULT 7

Q6DCM4 PRELIMINARY; PRT; 313 AA.
ID Q6DCM4
AC Q6DCM4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Spond2-prov protein.
GN Name=spond2-prov;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]

SEQUENCE FROM N.A.
 TISSUE=Embryo;
 MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 Richardson P.;
 "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 initiative";
 Dev. Dyn. 225:384-391(2002).
 [2]
 SEQUENCE FROM N.A.
 TISSUE=Embryo;
 PubMed=12477932; DOI=10.1073/pnas.242603899;
 Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.F., Schuler G.D.,
 Altschul S.F., Zengberg B., Buetow K.H., Schaefer C.W., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S.C., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 Krzywinski M.I., Skalka U., Smailus D.E., Schnerch A., Schein J.E.,
 Jones S.J., Marra M.A.;
 "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [3]
 SEQUENCE FROM N.A.
 TISSUE=Embryo;
 Klein S., Gerhard D.S.;
 Submitted (JUL-2004) to the EMBL/GenBank/DBSJ databases.
 ENBL; BC077984; AAH77984.1; -;
 CG; GO:0007155; P:cell adhesion; IEA.
 GO; GO:0007275; P:development; IEA.
 DR InterPro; IPR009465; Spnd_N.
 DR InterPro; IPR000884; TSPI.
 DR Pfam; PF06468; Spnd_N; 1.
 DR Pfam; PF00090; TSP 1; 1.
 DR SMART; SM00209; TSPI; 1.
 DR PROSITE; PS50092; TSPI; 1.
 SQ SEQUENCE 313 AA; 34476 MW; 686F610A18ED28E9 CRC64;
 Query Match 64.7%; Score 55; DB 2; Length 313;
 Best Local Similarity 66.7%; Pred. No. 0.93;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps
 Qy 1 HSSDYSWWRKNQYVS 15
 ||||| ||:| :||
 Db 61 HSSDYHWWKKLEPVS 75
 RESULT 8
 Q82UD3
 ID Q82UD3 PRELIMINARY; PRT; 138 AA.
 AC Q82UD3;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocuNames=NEI559;
 OS Nitrosomonas europaea.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
 OC Nitrosomonadaceae; Nitrosomonas.
 ON NCBI_TaxID=915;
 [1]
 RC SEQUENCE FROM N.A.
 RC STRAIN=ATCC 19718 / IFO 14298;

RX	MEDLINE=22586410; PubMed=12700255;	
RR	DOI=10.1128/JB.185.9.2759-2773.2003;	
RA	Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.L.,	
RA	Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,	
RA	Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.;	
RT	"Complete genome sequence of the ammonia-oxidizing bacterium and	
RT	obligate chemolithoautotroph Nitrosomonas europaea.";	
RL	J. Bacteriol. 185:2759-2773 (2003).	
RL	EMBL; BX321861; CAD85470.1; -;	
KW	Complete proteome; Hypothetical protein.	
KW	SEQUENCE 138 AA; 15572 MW; 54326051C08B07C6 CRC64;	
QY	1 HSDYSMRKNQYV 14	
DB	39 HASDQSLMSDTQYV 52	
	I: : : : :	
	I: : : : :	
RESULT 9		
ID	Q22019 PRELIMINARY; PRT; 420 AA.	
AC	Q22019;	
DT	01-JAN-1998 (TrEMBLrel. 05, Created)	
DT	01-JAN-1998 (TrEMBLrel. 05, Last sequence update)	
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)	
DE	ORF420.	
OS	Cyanidioschyzon merolae (Red alga).	
OC	Eukaryota; Rhodophyta; Bangiophyceae; Cyanidiales; Cyanidiaceae;	
OC	Cyanidioschyzon.	
OX	NCBI_TaxID=45157;	
OX	11	
RP	SEQUENCE FROM N.A.	
RA	Ohta N.;	
RT	"Analysis of a plastid gene cluster reveals a close relationship	
RT	between Cyanidioschyzon and Cyanidium.";	
RT	J. Plant Res. 110:235-245 (1997).	
DR	EMBL; D631675; BAA22815.1; -;	
DR	GO; GO:0005525; F:GTP binding; IEA.	
DR	GO; GO:0003743; F:translation initiation factor activity; IEA.	
DR	GO; GO:0006413; P:translational initiation; IEA.	
DR	InterPro; IPR000178; IP2.	
DR	InterPro; IPR009000; Translat_factor.	
DR	Pfam; PF04760; IP2_N; 1.	
DR	PRODOM; PDI86100; IP2; 1.	
SQ	SEQUENCE 420 AA; 47691 MW; A6CAE107B24B4E19 CRC64;	
	Query Match 57.6%; Score 49; DB 2; Length 420;	
	Best Local Similarity 70.0%; Pred. No. 12;	
	Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps	
QY	4 DYSMRKNQY 13	
DB	366 EYEINRKNQY 375	
	I: : : :	
	I: : : :	
RESULT 10		
Q85G84		
ID	Q85G84 PRELIMINARY; PRT; 446 AA.	
AC	Q85G84;	
DT	01-JUN-2003 (TrEMBLrel. 24, Created)	
DT	01-JUN-2003 (TrEMBLrel. 24, Last sequence update)	
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)	
DE	Initiation factor 2.	
GN	Name=infB;	
OS	Cyanidioschyzon merolae (Red alga).	
OC	Chloroplast.	
OC	Eukaryota; Rhodophyta; Bangiophyceae; Cyanidiales; Cyanidiaceae;	
OC	Cyanidioschyzon.	
OX	NCBI_TaxID=45157;	

```
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=10D;
RA MEDLINE=22639682; PubMed=12755171;
RA Ohta N., Matsuaki M., Misumi O., Miyagishima S., Nozaki H.,
RA Tanaka K., Shin-i T., Kohara Y., Kuroiwa T.;
RT "Complete Sequence and Analysis of the Plastid Genome of the
RT Unicellular Red Alga Cyanidioschyzon merolae.";
RL DNA Res. 10:67-77(2003).
DR EMBL: AB002583; BAC76102.1; -.
DR GO: GO:0005907; C:chloroplast; IEA.
DR GO: GO:0005255; F:GTP binding; IEA.
DR GO: GO:0003743; F:translation initiation factor activity; IEA.
DR GO: GO:0006413; P:translational initiation; IEA.
DR InterPro: IPR00178; IPF2.
DR InterPro: IPR006847; IPF2_N.
DR InterPro: IPR009000; Translat_factor.
DR Pfam: PF04760; IPF2_N; 1.
DR ProDom: PD186100; IPF2; 1.
KW Chloroplast; Initiation factor.
SQ SEQUENCE 446 AA; 50850 MW; 89A8BD5483020527 CRC64;
```

```
Query Match 57.6%; Score 49; DB 2; Length 446;
Best Local Similarity 70.0%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 4 DYSWKRKNQY 13
      :|:|||||
Db 392 EYIWRKNQY 401
```

```
RESULT 11
ID Q7Y4U7 PRELIMINARY; PRT; 390 AA.
AC Q7Y4U7;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Gp27 baseplate hub subunit.
OS Bacteriophage RB69.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC T4-like viruses.
OC NCBI_TaxID=12353;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98215164; PubMed=9555879;
RA Yeh L.S., Hsu T., Karam J.D.;
RT "Divergence of a DNA replication gene cluster in the T4-related
RT bacteriophage RB69.";
RL J. Bacteriol. 180:2005-2013(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20566703; PubMed=11114936; DOI=10.1128/JB.183.1.358-366.2001;
RA Tetart F., Desplats C., Kutateladze M., Monod C., Ackermann H.W.,
RA Krisch H.M.;
RT "Phylogeny of the major head and tail genes of the wide-ranging T4-
RT type bacteriophages.";
RL J. Bacteriol. 183:358-366(2001).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=96064739; PubMed=7592876; DOI=10.1074/jbc.270.44.26558;
RA Wang C.C., Yeh L.S., Karam J.D.;
RT "Modular organization of T4 DNA polymerase. Evidence from
RT phylogenetics.";
RL J. Biol. Chem. 270:26558-26564(1995).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=97358535; PubMed=9215631; DOI=10.1016/S0092-8674(00)80296-2;
RA Wang J., Sattar A.K., Wang C.C., Karam J.D., Konigsberg W.H.,
RA Steitz T.A.;
RT "Crystal structure of a pol alpha family replication DNA polymerase
RT from bacteriophage RB69.";
RL Cell 89:1087-1099(1997).
```

```
RN [5]
RP SEQUENCE FROM N.A.
RA Borjac J., Petrov V.M., Karam J.D.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RA Petrov V., Nolan J., Chin D., Letarov A., Krisch H.M., Karam J.D.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY303349; AAP76103.1; -.
SQ SEQUENCE 390 AA; 44285 MW; C0523000DD657817 CRC64;
```

```
Query Match 55.3%; Score 47; DB 2; Length 390;
Best Local Similarity 63.6%; Pred. No. 24;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 4 DYSWKRKNQYV 14
      |||||:|:|:|
Db 19 DYSAWQENRYV 29
```

```
RESULT 12
AMYL_HORVU
ID AMYL_HORVU STANDARD; PRT; 438 AA.
AC P00693;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Alpha-amylase type A isozyme precursor (EC 3.2.1.1) (1,4-alpha-D-
DE Glucan glucanohydrolase) (AMYL) (Low pI alpha-amylase).
DE Name=AMYL1;
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Hordeum.
OC NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Himalaya;
RX MEDLINE=83238423; PubMed=6190808;
RA Rogers J.C., Millman C.;
RT "Isolation and sequence analysis of a barley alpha-amylase cDNA
RT clone.";
RL J. Biol. Chem. 258:8169-8174(1983).
RN [2]
RP MUTAGENESIS OF HIS-117; ASP-204; GLU-229; TRP-303; HIS-314 AND
RP ASP-315.
RX PubMed=7901200;
RA Sogaard M., Kadziola A., Haer R., Svensson B.;
RT "Site-directed mutagenesis of histidine 93, aspartic acid 180,
RT glutamic acid 205, histidine 290, and aspartic acid 291 at the active
RT site and tryptophan 279 at the raw starch binding site in barley
RT alpha-amylase 1.";
RL J. Biol. Chem. 268:22480-22484(1993).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 25-428.
RX PubMed=12906828;
RA Robert X., Haer R., Gottschalk T.E., Ratajczak F., Driguez H.,
RA Svensson B., Aghajari N.;
RT "The structure of barley alpha-amylase isozyme 1 reveals a novel role
RT of domain C in substrate recognition and binding: a pair of sugar
RT tongs.";
RL Structure 11:973-984(2003).
CC -I- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -I- COPACTOR: Binds 3 calcium ions per subunit (By similarity).
CC -I- SUBUNIT: Monomer (By similarity).
CC -I- SUBCELLULAR LOCATION: Extracellular.
CC -I- DEVELOPMENTAL STAGE: Production of alpha-amylase is hormonally
CC regulated. Germinating embryos produce the hormone gibberellic
CC acid, which within 10 hours stimulates the aleurone cells covering
CC the endosperm of the seed to produce alpha-amylase. The enzyme
CC then degrades the starch within the endosperm for use by the
CC developing plant embryo.
```



```

KW Nuclear protein.
SQ SEQUENCE 1453 AA; 164938 MW; ELC3DA8556FA406E CRC64;

Query Match      54.1%; Score 46; DB 2; Length 1453;
Best Local Similarity 54.5%; Pred. No. 1.4e+02;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy      1 HSDYSMWRKN 11
      |::|::|::|
Db      990 HNASYAVWRKN 1000

RESULT 15
Q9GRL1
ID Q9GRL1 PRELIMINARY; PRT; 845 AA.
AC Q9GRL1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein P214.31.
OS Name=P214.31;
GN Leishmania major.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Friedlin;
RX MEDLINE=98146435; PubMed=9477341;
RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
RA Smith D.F.;
RT "A physical map of the Leishmania major Friedlin genome.";
RL Genome Res. 8:135-145(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Friedlin;
RA Saunders D., Murphy L., Harris D., Ivens A.C., Quail M.,
RA Rajandream M.A., Barrell B.G.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL449144; CAC14638.1; -
DR InterPro; IPR000626; Ubiquitin.
DR Pfam; PF00240; ubiquitin; 1.
DR SMART; SM00213; UBQ; 1.
DR PROSITE; PS50053; UBIQUITIN_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 845 AA; 89557 MW; 57CA41EA2D94A5B2 CRC64;

Query Match      52.9%; Score 45; DB 2; Length 845;
Best Local Similarity 53.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy      1 HSDYSMWRKNQY 13
      |||::|::|
Db      826 HSGDWNWEANPY 838

Search completed: June 3, 2005, 08:28:08
Job time : 16.1 secs

```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 3, 2005, 07:49:16 ; Search time 15.825 Seconds
(without alignments)
366.598 Million cell updates/sec

Title: US-10-616-279-10

Perfect score: 85

Sequence: 1 HSSDYSNWRKNQVVS 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	100.0	15	4 AAB82474	Aab82474 Human ext
2	85	100.0	290	2 AAW83329	Aaw83329 Human min
3	85	100.0	330	4 AAE12304	Aae12304 Human NPG
4	85	100.0	331	2 AAW23663	Aaw23663 Human neu
5	85	100.0	331	2 AAW70589	Aaw70589 Adhesion-
6	85	100.0	331	2 AAW83328	Aaw83328 Human min
7	85	100.0	331	2 AAY41721	Aay41721 Human PRO
8	85	100.0	331	2 AAW92460	Aaw92460 Human NAF
9	85	100.0	331	3 AAB33465	Aab33465 Human PRO
10	85	100.0	331	3 AAY79561	Aay79561 Cancer sp
11	85	100.0	331	3 AAB44277	Aab44277 Human PRO
12	85	100.0	331	3 AAY95349	Aay95349 Human PRO
13	85	100.0	331	4 AAM93266	Aam93266 Human pol
14	85	100.0	331	4 AAM93324	Aam93324 Human pol
15	85	100.0	331	4 AAM38872	Aam38872 Human pol
16	85	100.0	331	4 AAB82472	Aab82472 Human ext
17	85	100.0	331	5 ABG61806	Abg61806 Prostate
18	85	100.0	331	5 AAU79944	Aau79944 Human Spo
19	85	100.0	331	5 ABB77393	Abb77393 Human spo
20	85	100.0	331	5 AAE20463	Aae20463 Human tum
21	85	100.0	331	6 ABO25223	AbO25223 Novel hum
22	85	100.0	331	6 ABU72229	Abu72229 Novel hum
23	85	100.0	331	6 ABU84909	Abu84909 Human sec
24	85	100.0	331	6 ABU61107	Abu61107 Human PRO
25	85	100.0	331	6 ABU80376	Abu80376 Human sec

26	85	100.0	331	6 ABG75949	Abg75949 Human ant
27	85	100.0	331	6 ADA24775	Ada24775 Novel hum
28	85	100.0	331	6 ABO19678	AbO19678 Novel hum
29	85	100.0	331	6 ADA12436	Ada12436 Human sec
30	85	100.0	331	6 ABO19569	AbO19569 Novel hum
31	85	100.0	331	7 ADB73742	Adb73742 Human PRO
32	85	100.0	331	7 ADB76458	Adb76458 Human PRO
33	85	100.0	331	7 ADB75561	Adb75561 Prostate
34	85	100.0	331	7 ADC43884	Adc43884 Human sec
35	85	100.0	331	7 ADC61644	Adc61644 Human sec
36	85	100.0	331	7 ADC63608	Adc63608 Human sec
37	85	100.0	331	7 ADC66708	Adc66708 Human sec
38	85	100.0	331	7 ADC68832	Adc68832 Human sec
39	85	100.0	331	7 ADC82892	Adc82892 Human sec
40	85	100.0	331	7 ADC67957	Adc67957 Human sec
41	85	100.0	331	7 ADC41277	Adc41277 Human sec
42	85	100.0	331	7 ADC67332	Adc67332 Human sec
43	85	100.0	331	7 ADC62268	Adc62268 Human sec
44	85	100.0	331	7 ADC41901	Adc41901 Human sec
45	85	100.0	331	7 ADE49270	Ade49270 Human sec

ALIGNMENTS

RESULT 1

AAB82474

ID AAB82474 standard; peptide; 15 AA.

XX

AC AAB82474;

XX

DT 22-AUG-2001 (first entry)

XX

DE Human extracellular matrix protein RGI immunogenic peptide 3C.

XX

KW RGI; human; extracellular matrix protein; prostate cancer; metastasis; tumour; benign prostatic hyperplasia; therapy; diagnosis; antitumour; immunogen.

XX

OS Homo sapiens.

XX

PN WO200144291-A2.

XX

PD 21-JUN-2001.

XX

PF 15-DEC-2000; 2000WO-US033901.

XX

PR 16-DEC-1999; 99US-0172370P.

PR

PR 07-DEC-2000; 2000US-00732357.

XX

(SCHD) SCHERING AG.

XX

Harkins R, Parkes D, Parry G, Schneider DW, Steinbrecher R;

XX

WFI; 2001-398128/42.

XX

Novel human extracellular matrix polypeptide, RGI, useful in research, diagnosis and treatment of metastasis such as prostate cancer.

XX

Claim 26; Page 48; 69pp; English.

XX

The present sequence is that of immunogenic peptide 3C of human RGI (see AAB82472). RGI is a new homologue of the extracellular matrix protein family that is expressed in prostate tissue and which may be over-expressed in prostate tumours. Peptide 3C corresponds to amino acid residues 77-91 of RGI. It was selected as a potential immunogen because of its predicted position at the surface of the protein. Antisera raised against peptide 3C recognise RGI. An antibody that specifically binds to the peptide is claimed. The invention provides human RG polypeptides, polynucleotides encoding them, and antibodies which specifically bind RGI or a polypeptide such as the present sequence. Such antibodies can be used for diagnosis and/or detection of RGI expression, or can be conjugated (e.g. as an Fv, F(ab')₂ fragment) to a therapeutic

CC agent, especially a cytotoxic agent, for administration to a patient for
 CC treatment of diseases characterised by Rgl activity or expression, such
 CC as prostate cancer

SQ Sequence 15 AA;
 Query Match 100.0%; Score 85; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.2e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HSSDYSWVRKNQYVS 15
 |||||
 Db 1 HSSDYSWVRKNQYVS 15

RESULT 2
 AAW83329
 ID AAW83329 standard; protein; 290 AA.
 XX AC AAW83329;
 XX DT 01-MAR-1999 (first entry)
 XX DE Human mindin-related polypeptide.
 XX Mindin; human; integrin ligand; angiogenic disease; cancer; metastasis;
 KW chronic inflammatory disorder; rheumatoid arthritis; atherosclerosis;
 KW macular degeneration, diabetic retinopathy; restenosis;
 KW Alzheimer's disease; neural disorder; tissue remodelling; therapy;
 KW diagnosis.
 XX OS Homo sapiens.
 XX PN W09850073-A1.
 XX PD 12-NOV-1998.
 XX PF 07-MAY-1998; 98WO-US009476.
 XX PR 09-MAY-1997; 97US-0046106P.
 XX PA (SMIK) SMITHKLINE BEECHAM CORP.
 XX PI Jonak ZL, Trulli SH, Tsui P, Lane PA;
 XX WPI: 1999-034688/03.
 XX N-PSDB; AAV72538.

A new polypeptide is the integrin ligand, human mindin - useful in
 therapy and diagnostic assays for diseases such as those associated with
 angiogenesis.

Claim 14; Page 30-31; 39pp; English.
 This amino acid sequence was deduced from the nucleotide sequence (see
 AAV72538) of expressed sequence tags identified prior to the isolation of
 a full-length sequence (see AAV72537) encoding human mindin (see
 AAW83328). Claimed polypeptides have an amino acid sequence which has at
 least 70%, 80%, 90%, 95% or 97-77% identity to this polypeptide, or
 comprise the amino acid sequence of the polypeptide itself, or are
 encoded by a polynucleotide comprising the sequence contained in
 AAV72538. The invention relates to human mindin polypeptides and
 polynucleotides (see also AAV72537). Mindin is a novel integrin ligand
 suggested to have multifunctional activity in normal and disease states.
 Methods are provided for using mindin polypeptides and polynucleotides in
 the treatment and diagnosis of angiogenic diseases (cancer, cancer
 metastasis, chronic inflammatory disorders, rheumatoid arthritis,
 atherosclerosis, macular degeneration, diabetic retinopathy), restenosis,
 Alzheimer's disease, neural disorders and tissue remodelling. The
 invention also relates to methods for identifying agonists and
 antagonists/inhibitors and for treating conditions associated with human
 mindin imbalance with the identified compounds. Diagnostic assays for
 detecting diseases associated with inappropriate human mindin activity or

CC levels are also claimed
 XX Sequence 290 AA;
 SQ

Query Match 100.0%; Score 85; DB 2; Length 290;
 Best Local Similarity 100.0%; Pred. No. 9.1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HSSDYSWVRKNQYVS 15
 |||||
 Db 77 HSSDYSWVRKNQYVS 91

RESULT 3
 AAE12304
 ID AAE12304 standard; protein; 330 AA.
 XX AC AAE12304;
 XX DT 03-JAN-2002 (first entry)
 XX DE Human NPG-1 protein.
 XX Human; NPG-1; cytostatic; gene therapy; tumour; prostate cancer; LCS;
 KW Linker Capture Subtraction; genetic alteration; nerve cell growth.
 XX OS Homo sapiens.
 XX PN US6287777-B1.
 XX PD 11-SEP-2001.
 XX PF 10-AUG-1999; 99US-00371696.
 XX PR 10-MAY-1996; 96US-00644326.
 XX PD 11-FEB-1998; 98US-00022238.
 XX (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
 XX Sytkowski AJ, Yang M;
 XX WPI: 2001-624488/72.
 XX N-PSDB; AAD20094.

Detecting the presence of a nucleic acid encoding NPG-1 in a sample
 comprises contacting the sample with a nucleic acid probe or primer which
 hybridizes under stringent conditions to NPG-1 nucleic acid.

Example; Fig 2; 35pp; English.

The invention relates to a method termed Linker Capture Subtraction (LCS)
 for detecting the presence of a nucleic acid encoding NPG-1. NPG-1 gene
 is differentially expressed in prostate tumours. The method is used for
 identifying nucleic acids encoding NPG-1. NPG-1 can be used for treating
 a subject having a tumour, cancer, for the adhesion and outgrowth of
 axon, for stimulating growth of nerve cell, and regenerating nerve cells.
 The NPG-1 nucleic acids, protein and antibodies may be used in screening
 assays, detecting assays, and predictive medicine. The nucleic acids are
 further used to express an NPG-1 protein, to detect NPG-1 mRNA or a
 genetic alteration in an NPG-1 gene, and to modulate NPG-1 activity. The
 present sequence is human NPG-1 protein

Sequence 330 AA;

Query Match 100.0%; Score 85; DB 4; Length 330;
 Best Local Similarity 100.0%; Pred. No. 1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HSSDYSWVRKNQYVS 15
 |||||
 Db 77 HSSDYSWVRKNQYVS 91

RESULT 4

AAW23663 ID AAW23663 standard; protein; 331 AA.

XX AC AAW23663;

XX DT 08-MAR-1998 (first entry)

XX DE Human neuronal attachment factor-1.

XX DE Neuronal attachment factor-1; NAF-1; human; cell-cell interaction;
KW cell adhesion; spinal cord injury; peripheral nerve damage; tumour;
KW metastasis; therapy; malaria; wound healing.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
XX Peptide 1. 23

XX FT /label= Sig_peptide

XX FT Protein 24. 331

XX FT /label= Mat_protein

XX PN WO9729189-A1.

XX PD 14-AUG-1997.

XX PF 12-FEB-1996; 96WO-US001857.

XX PR 12-FEB-1996; 96WO-US001857.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Hastings GA;

XX DR WPI; 1997-415344/38.

XX DR N-PSDB; AAT78360.

XX PT New isolated human neuronal attachment factor-1 - promotes cell-cell
PT interaction and cell adhesion, used for treating e.g. spinal cord injury,
PT peripheral nerve damage or tumours.

XX PS Claim 1; Page 42-43; 55pp; English.

XX CC This protein comprises human neuronal attachment factor-1 (NAF-1), a
CC novel protein that promotes cell-cell interaction and cell adhesion. Its
CC amino acid sequence was deduced from a DNA molecule (see AAT78360)
CC isolated from a cDNA library derived from human epithelial sarcoma. NAF-1
CC shows sequence homology to the rat F-spondin family. NAF-1 polypeptides,
CC especially the mature protein, can be expressed in host cells. It can be
CC used e.g. to treat spinal cord injuries or damage to peripheral nerves by
CC promoting neural cell adhesion and neurite extension, to inhibit tumour
CC cell metastases, inhibit endothelial cell proliferation, adhesion and
CC motility, to decrease tumour neovascularisation, to be angiostatic for
CC tumours, to promote wound healing, and to modulate haemostasis. It can
CC also be used to screen for agonists and for antagonists useful e.g. in
CC the prevention of malaria

XX SQ Sequence 331 AA;

Query Match 100.0%; Score 85; DB 2; Length 331;

Best Local Similarity 100.0%; Pred. No. 1e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HSSDYSWVRKNQYVS 15

|||||

Db 77 HSSDYSWVRKNQYVS 91

RESULT 5

AAW70589 ID AAW70589 standard; protein; 331 AA.

XX AC AAW70589;

XX DT

XX DE 21-JAN-1999 (first entry)

XX DE Adhesion-modulating protein zsig25.

XX KW zsig25; adhesion-modulating protein; prostate cell; prostatic carcinoma;
KW B-cell cancer; infertility; Wolf-Hirschhorn syndrome;
KW chromosome 4 (p16.3).

XX OS Homo sapiens.

XX PN WO9845442-A2.

XX PD 15-OCT-1998.

XX PF 10-APR-1998; 98WO-US007117.

XX PR 10-APR-1997; 97US-0043421P.

XX PR 11-JUN-1997; 97US-0049288P.

XX PA (ZYMO) ZYMOGENETICS INC.

XX PI Sheppard PO;

XX DR WPI; 1998-557522/47.

XX DR N-PSDB; AAV63241.

XX PT New zsig25 protein - and antibodies, involved in modulation of adhesion,
PT used for diagnosis and treatment of prostatic and B-cell tumours,
PT stimulation of haematopoietic cells, treatment of immune deficiency etc.

XX PS Claim 7; Page 111; 161pp; English.

XX CC The present sequence represents a protein designated zsig25. The zsig25
CC protein is an adhesion-modulating protein expressed at very high level in
CC prostate cells. The protein is useful as a diagnostic marker for
CC prostatic carcinoma and B-cell cancers, possibly also for infertility,
CC and as a reagent for separating cancerous and non-cancerous cells. The
CC products may also be used to diagnose or treat Wolf-Hirschhorn syndrome,
CC associated with a deletion in the region of chromosome 4 (p16.3) where
CC the zsig25 gene is located

XX SQ Sequence 331 AA;

Query Match 100.0%; Score 85; DB 2; Length 331;

Best Local Similarity 100.0%; Pred. No. 1e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HSSDYSWVRKNQYVS 15

|||||

Db 77 HSSDYSWVRKNQYVS 91

RESULT 6

AAW83328

ID AAW83328 standard; protein; 331 AA.

XX AC AAW83328;

XX DT 01-MAR-1999 (first entry)

XX DE Human mindin polypeptide.

XX KW Mindin; human; integrin ligand; angiogenic disease; cancer; metastasis;
KW chronic inflammatory disorder; rheumatoid arthritis; atherosclerosis;
KW macular degeneration, diabetic retinopathy; restenosis;
KW Alzheimer's disease; neural disorder; tissue remodelling; therapy;
KW diagnosis.

XX OS Homo sapiens.

XX PN WO9850073-A1.

XX DT

PD 12-NOV-1998.
XX
PF 07-MAY-1998; 98WO-US009476.
XX
XX 09-MAY-1997; 97US-0046106P.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
XX Jonak ZL, Trulli SH, Tsui F, Lane PA;
XX
XX WPI; 1999-034688/03.
DR N-PSDB; AAV72537.
XX
XX A new polypeptide is the integrin ligand, human mindin - useful in
PT therapy and diagnostic assays for diseases such as those associated with
PT angiogenesis.
XX
XX Claim 1; Page 29; 39pp; English.
XX
XX This is the amino acid sequence of human mindin, a novel integrin ligand.
CC It has homology to F spondin, and may have a multifunctional activity in
CC normal and disease states. The invention provides human mindin
CC polypeptides and polynucleotides (see also AAV72537-38) and methods for
CC producing such polypeptides by recombinant techniques. It also relates to
CC methods for using such polypeptides and polynucleotides in the treatment
CC of angiogenic diseases (cancer, cancer metastasis, chronic inflammation,
CC disorders, rheumatoid arthritis, atherosclerosis, macular degeneration,
CC diabetic retinopathy), restenosis, Alzheimer's disease, neural disorders
CC and tissue remodelling. The invention also relates to methods for
CC identifying agonists and antagonists/inhibitors and for treating
CC conditions associated with human mindin imbalance with the identified
CC compounds. Diagnostic assays for detecting diseases associated with
CC inappropriate human mindin activity or levels are also claimed
XX
XX Sequence 331 AA;
SQ
Query Match 100.0%; Score 85; DB 2; Length 331;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HSSDYSMWKKNQYVS 15
Db 77 HSSDYSMWKKNQYVS 91
RESULT 7
AAV41721
ID AAV41721 standard; protein; 331 AA.
XX
XX AAV41721;
XX
XX 07-DEC-1999 (first entry)
DT
DE Human PRO866 protein sequence.
XX
XX Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
KW secreted protein; transmembrane protein.
XX
XX Homo sapiens.
OS
XX
XX WO9946281-A2.
XX
XX 16-SEP-1999.
PD
XX 08-MAR-1999; 99WO-US005028.
PF
XX 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077641P.
PR 11-MAR-1998; 98US-0077649P.
PR 12-MAR-1998; 98US-0077791P.
PR 13-MAR-1998; 98US-0078004P.
PR
PR 17-MAR-1998; 98US-00040220.
PR 20-MAR-1998; 98US-0078866P.
PR 20-MAR-1998; 98US-0078910P.
PR 20-MAR-1998; 98US-0078936P.
PR 20-MAR-1998; 98US-0078939P.
PR 25-MAR-1998; 98US-0079294P.
PR 26-MAR-1998; 98US-0079656P.
PR 26-MAR-1998; 98US-0079663P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079689P.
PR 27-MAR-1998; 98US-0079728P.
PR 27-MAR-1998; 98US-0079786P.
PR 30-MAR-1998; 98US-0079920P.
PR 30-MAR-1998; 98US-0079923P.
PR 31-MAR-1998; 98US-0080105P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080165P.
PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080328P.
PR 01-APR-1998; 98US-0080333P.
PR 01-APR-1998; 98US-0080334P.
PR 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
PR 08-APR-1998; 98US-0081071P.
PR 09-APR-1998; 98US-0081195P.
PR 09-APR-1998; 98US-0081203P.
PR 09-APR-1998; 98US-0081229P.
PR 15-APR-1998; 98US-0081817P.
PR 15-APR-1998; 98US-0081838P.
PR 15-APR-1998; 98US-0081952P.
PR 15-APR-1998; 98US-0081955P.
PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082700P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082804P.
PR 23-APR-1998; 98US-0082767P.
PR 23-APR-1998; 98US-0082796P.
PR 27-APR-1998; 98US-0083336P.
PR 28-APR-1998; 98US-0083322P.
PR 28-APR-1998; 98US-0083392P.
PR 29-APR-1998; 98US-0083495P.
PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083499P.
PR 29-APR-1998; 98US-0083500P.
PR 29-APR-1998; 98US-0083545P.
PR 29-APR-1998; 98US-0083558P.
PR 29-APR-1998; 98US-0083559P.
PR 30-APR-1998; 98US-0083742P.
PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
PR 06-MAY-1998; 98US-0084441P.
PR 07-MAY-1998; 98US-0084598P.
PR 07-MAY-1998; 98US-0084600P.
PR 07-MAY-1998; 98US-0084627P.
PR 07-MAY-1998; 98US-0084637P.
PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
PR 07-MAY-1998; 98US-0084643P.
PR 13-MAY-1998; 98US-0085323P.
PR 13-MAY-1998; 98US-0085338P.
PR 13-MAY-1998; 98US-0085339P.
PR 15-MAY-1998; 98US-0085573P.
PR 15-MAY-1998; 98US-0085579P.
PR 15-MAY-1998; 98US-0085580P.
PR 15-MAY-1998; 98US-0085582P.
PR 15-MAY-1998; 98US-0085689P.
PR 15-MAY-1998; 98US-0085697P.
PR 15-MAY-1998; 98US-0085700P.
PR 15-MAY-1998; 98US-0085704P.
PR 18-MAY-1998; 98US-0086023P.
PR

PR 22-MAY-1998; 98US-0086392P.
 PR 22-MAY-1998; 98US-0086414P.
 PR 22-MAY-1998; 98US-0086430P.
 PR 28-MAY-1998; 98US-0086486P.
 PR 28-MAY-1998; 98US-0087098P.
 PR 28-MAY-1998; 98US-0087106P.
 PR 28-MAY-1998; 98US-0087208P.
 PR 30-JUL-1998; 98US-0094651P.
 PR 11-SEP-1998; 98US-0100038P.
 XX (GETH) GENENTECH INC.
 XX
 PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
 XX
 DR WPI; 1999-551358/46.
 DR N-PSDB; AAZ34089.
 XX
 XX New secreted and transmembrane polypeptides and their polynucleotides,
 PT useful for treating blood coagulation disorders, cancers and cellular
 PT adhesion disorders.
 XX
 PS Claim 12; Fig 87; 530pp; English.
 XX
 CC The present invention describes secreted and transmembrane polypeptides
 CC and their polynucleotides. The nucleotide sequences are useful as sources
 CC of probes, primers, for chromosome mapping, and for generation of
 CC antisense sequences. They can also be used to create transgenic animals.
 CC The proteins can be used to treat a variety of diseases and disorders,
 CC depending on their function. Diseases that may be treated include blood
 CC coagulation disorders, cancers and cellular adhesion disorders. They may
 CC also be used to raise antibodies. AAZ33891 to AAZ34338, and AAY41685 to
 CC AAY41774 represent polynucleotide and polypeptide sequence given in the
 CC exemplification of the present invention
 XX
 SQ Sequence 331 AA;
 Query Match 100.0%; Score 85; DB 2; Length 331;
 Best Local Similarity 100.0%; Pred. No. 1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HSSDYSWMRKQYVS 15
 |||||
 Db 77 HSSDYSWMRKQYVS 91
 RESULT 8
 ID AAW92460
 AC AAW92460; standard; protein; 331 AA.
 XX
 DT 21-APR-1999 (first entry)
 XX
 DE Human NAP-1 protein.
 XX
 KW NAP-1; neuronal attachment factor-1; F-spondin analogue; treatment;
 KW spinal cord injury; peripheral nerves damage; neural cell adhesion;
 KW neurite extension; tumour cell metastasis; inhibitor; mobility; disease;
 KW endothelial cell proliferation; tumour neovascularisation; haemostasis;
 KW angiostatic agent; wound healing; diagnostic; neurotrophic; anticancer;
 KW antimetastatic; anti-angiogenic; antimalarial; human.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..23
 FT /label= signal_peptide
 FT Protein 24..331
 XX
 XX US5871969-A.
 XX
 PD 16-FEB-1999.
 XX

PF 12-FEB-1997; 97US-00799173.
 PR 12-FEB-1996; 96US-0011519P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Dillon PJ, Hastings G;
 XX
 DR WPI; 1999-166644/14.
 DR N-PSDB; AAX02019.
 XX
 XX Nucleic acid encoding human neuronal attachment factor-1 - used to e.g.
 PT treat spinal cord injuries, and inhibit tumor cell metastasis and
 PT neovascularization.
 XX
 PS Claim 1a; Fig 1; 29pp; English.
 XX
 CC This sequence represents a novel human neuronal attachment factor-1, NAP-
 CC 1. NAP-1 is an analogue of rat F-spondin and is used to treat spinal cord
 CC injuries and damage to peripheral nerves (by promoting neural cell
 CC adhesion and neurite extension), to inhibit tumor cell metastasis
 CC (particularly in small cell and breast carcinoma) and endothelial cell
 CC proliferation, adhesion and mobility, to reduce tumor neovascularisation,
 CC as angiostatic agents for tumor cells, to promote wound healing and to
 CC modulate hemostasis. NAP-1 may also be used to identify treatments and
 CC diagnoses for human disease. Fragments of the nucleic acid that do not
 CC encode NAP-1 peptides are useful as probes to isolate the NAP-1 gene, its
 CC allelic variants, full-length cDNA or related sequences, in chromosomal
 CC location by in situ hybridization or in Northern blotting, and as
 CC diagnostic probes or primers. The protein has neurotrophic, anticancer,
 CC antimetastatic, anti-angiogenic, antimalarial and modulates adhesion,
 CC proliferation and mobility of cells
 XX
 SQ Sequence 331 AA;
 Query Match 100.0%; Score 85; DB 2; Length 331;
 Best Local Similarity 100.0%; Pred. No. 1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HSSDYSWMRKQYVS 15
 |||||
 Db 77 HSSDYSWMRKQYVS 91
 RESULT 9
 ID AAB33465
 AC AAB33465; standard; protein; 331 AA.
 XX
 DT 29-JAN-2001 (first entry)
 XX
 DE Human PRO866 protein UNQ435 SEQ ID NO:258.
 XX
 KW Human; immune related disease; diagnosis; antiinflammatory; cardiant;
 KW dermatological; antiarthritic; antirheumatic; immunosuppressive;
 KW haemostatic; antithyroid; antidiabetic; neurotrophic; neuroprotective;
 KW antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;
 KW osteoarthritis; systemic lupus erythematosus; rheumatoid arthritis;
 KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
 KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
 KW autoimmune thrombocytopaenia; immune-mediated renal disease;
 KW demyelinating disease; hepatobiliary disease; Whipple's disease;
 KW inflammatory bowel disease; gluten-sensitive enteropathy;
 KW autoimmune disease; immune-mediated skin disease; allergic disease;
 KW immunological disease; transplantation associated disease;
 KW graft rejection; graft-versus-host-disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200053758-A2.
 XX

PD 14-SEP-2000.
 XX 02-MAR-2000; 2000WO-US005941.
 XX 08-MAR-1999; 99WO-US005028.
 PR 10-MAR-1999; 99US-0123618P.
 PR 12-MAR-1999; 99US-0123957P.
 PR 23-MAR-1999; 99US-0125775P.
 PR 12-APR-1999; 99US-0128849P.
 PR 20-APR-1999; 99WO-US008615.
 PR 28-APR-1999; 99US-0131445P.
 PR 04-MAY-1999; 99US-0132371P.
 PR 14-MAY-1999; 99US-0134287P.
 PR 02-JUN-1999; 99WO-US012252.
 PR 23-JUN-1999; 99US-0141037P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145638P.
 PR 28-JUL-1999; 99US-0146222P.
 PR 01-SEP-1999; 99WO-US020111.
 PR 08-SEP-1999; 99WO-US020594.
 PR 13-SEP-1999; 99WO-US020944.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 03-OCT-1999; 99WO-US023089.
 PR 29-OCT-1999; 99US-0162506P.
 PR 29-NOV-1999; 99WO-US028214.
 PR 30-NOV-1999; 99WO-US028313.
 PR 30-NOV-1999; 99WO-US028409.
 PR 01-DEC-1999; 99WO-US028301.
 PR 01-DEC-1999; 99WO-US028634.
 PR 02-DEC-1999; 99WO-US028551.
 PR 02-DEC-1999; 99WO-US028564.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030399.
 PR 30-DEC-1999; 99WO-US031274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 11-FEB-2000; 2000WO-US003376.
 PR 18-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 22-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 XX (GETH) GENENTECH INC.
 XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
 PI Kabakoff RC, Lu Y, Fan J, Pennica D, Shelton DL, Smith V;
 PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;
 XX WPI; 2000-572271/53.
 DR N-PSDB; AAC58630.
 XX Sixty four PRO polypeptides, useful in the diagnosis and treatment of
 PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
 PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus.
 XX
 PS Claim 33; Fig 104; 309pp; English.
 XX The present invention describes sixty four human PRO proteins which can
 CC be used in the treatment of immune related diseases. The human PRO
 CC proteins, anti-PRO antibodies, agonists and antagonists are useful for
 CC treating and diagnosing immune related disorders. The disorders are
 CC selected from systemic lupus erythematosus, rheumatoid arthritis,
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
 CC syndrome, autoimmune vasculitis, sarcoidosis, thyroiditis, diabetes mellitus,
 CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
 CC immune-mediated renal disease, demyelinating diseases of the central and
 CC peripheral nervous systems, hepatobiliary diseases, inflammatory bowel
 CC disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune
 CC or immune-mediated skin diseases, allergic diseases, immunological
 CC diseases of the lung, and transplantation associated diseases including

CC graft rejection and graft-versus-host-disease. AAC58397 to AAC58578
 CC represent PCR primers and hybridisation probes used in the isolation of
 CC human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477
 CC represent human PRO polynucleotide and protein sequences given in the
 CC exemplification of the present invention
 XX
 SQ Sequence 331 AA;
 Query Match 100.0%; Score 85; DB 3; Length 331;
 Best Local Similarity 100.0%; Pred. No. 1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 HSSDYSMWRKNQYVS 15
 Db 77 HSSDYSMWRKNQYVS 91
 RESULT 10
 AAY79561
 ID AAY79561 standard; protein; 331 AA.
 AC AAY79561;
 XX
 DT 15-AUG-2000 (first entry)
 XX
 DE Cancer specific protein Pro108 useful as prostate cancer marker.
 XX
 KW Cancer specific gene; CSG; prostate cancer; diagnosis; monitoring;
 KW staging; imaging; metastasis; therapy; human; Pro108.
 XX
 OS Homo sapiens.
 XX
 PN WO200023108-A1.
 XX
 PD 27-APR-2000.
 XX
 PF 18-OCT-1999; 99WO-US023764.
 XX
 PR 19-OCT-1998; 98US-0104741P.
 XX
 PA (DIAD-) DIADEXUS LLC.
 XX
 PI Ali SM, Sun Y, Salceda S, Recipon H, Cafferkey R;
 XX WPI; 2000-339528/29.
 DR N-PSDB; AAZ95034.
 XX
 PT Diagnosing, detecting, staging, monitoring, imaging and treating cancers,
 PT especially useful for detecting prostate cancer comprises measuring
 PT changes in levels of cancer specific genes in cells, tissues and body
 PT fluids.
 XX
 PS Claim 6; Page 29-30; 35pp; English.
 XX The present sequence is that of the protein encoded by human cancer
 CC specific gene (CSG) pro108 (see AAZ95034). The CSG was identified using a
 CC suppression subtractive hybridization method. It is a diagnostic marker
 CC for prostate cancer. In 11 different healthy tissues examined, pro108
 CC mRNA expression was highest in the ovary and uterus. Expression in
 CC healthy prostate was low. However, overexpression of CSG pro108 was
 CC observed in 13 of 13 prostate cancer tissues examined. CSGs comprising
 CC pro108, the encoded polypeptide, or an antibody that specifically binds
 CC CSG, are used in claimed methods for the diagnosis, detection, staging,
 CC monitoring, imaging and treatment of prostate cancer. The new methods
 CC provide earlier diagnosis for the presence and metastasis of prostate
 CC cancer, and can be used to determine if a cancer has metastasized, or to
 CC monitor the progress or stage of the disease when it has not metastasized
 XX
 SQ Sequence 331 AA;
 Query Match 100.0%; Score 85; DB 3; Length 331;
 Best Local Similarity 100.0%; Pred. No. 1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PI Napier MA, Pitti RM, Wood WI;
 XX WPI: 2000-442668/38.
 DR N-PSDB; AAA49728.
 XX
 PT Novel composition to inhibit neoplastic cell growth or for treating tumor
 PT in mammal comprises polypeptides PRO179, PRO207, PRO320, PRO219, PRO221,
 PT PRO224, PRO328, PRO301, PRO326, PRO356, PRO509 or PRO866.
 XX
 PS Claim 19; Fig 26; 172pp; English.
 XX
 CC The present sequence is that of human antitumour protein PRO866, as
 CC deduced from a foetal kidney cDNA clone (see AAA49728). PRO866 shows
 CC homology to members of the mindin/spondin family of proteins. A claimed
 CC method for inhibiting the growth of a tumour cell comprises exposing the
 CC tumor cell to PRO179, PRO207, PRO320, PRO219, PRO221, PRO224, PRO328,
 CC PRO301, PRO326, PRO362, PRO356, PRO509 or PRO866 (see AAY95337-49), their
 CC agonists or chimeric polypeptides incorporating them. The tumour is
 CC especially a cancer selected from breast, ovarian, renal, colorectal,
 CC uterine, prostate, lung, bladder and central nervous system cancer,
 CC melanoma and leukaemia. Methods for the recombinant expression of the
 CC antitumour proteins are also provided
 XX
 SQ Sequence 331 AA;
 Query Match 100.0%; Score 85; DB 3; Length 331;
 Best Local Similarity 100.0%; Pred. No. 1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HSSDYSWVRKNQYVS 15
 Db |||||
 77 HSSDYSWVRKNQYVS 91
 RESULT 13
 AAM93266
 ID AAM93266 standard; protein; 331 AA.
 AC
 XX AAM93266;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human polypeptide, SEQ ID NO: 2727.
 XX
 DE Human; full length cDNA; cDNA synthesis; oligo-capping.
 KW
 XX Homo sapiens.
 OS
 XX EP1130094-A2.
 PN
 XX 05-SEP-2001.
 PD
 XX 07-JUL-2000; 2000EP-00114089.
 PF
 XX 08-JUL-1999; 99JP-00194486.
 PR
 PR 11-JAN-2000; 2000JP-00118774.
 PR
 XX 02-MAY-2000; 2000JP-00183765.
 XX
 PA (HELI-) HELIX RES INST.
 XX
 XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
 XX
 XX WPI: 2001-524255/58.
 DR N-PSDB; AAK94182.
 DR
 XX
 XX 830 Primers useful for synthesizing full length cDNA clones and their use
 PT in genetic manipulation.
 PS Claim 8; SEQ ID NO 2727; 1380pp + Sequence Listing; English.
 XX
 CC The invention relates to primers for synthesizing full length cDNA
 CC clones. 830 cDNA molecules encoding a human protein have been isolated
 CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
 CC been determined. Primers for synthesizing the full length cDNA are useful
 CC for clarifying the function of the protein encoded by the cDNA. The full
 CC length clones were obtained by construction of full length enriched cDNA
 CC libraries that were synthesised by the oligo-capping method. The primers
 CC enable the production of the full length cDNA easily without any special
 CC methods. The present sequence is a polypeptide encoded by a full length
 CC human cDNA of the invention. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in CD-ROM
 CC format directly from EPO
 XX
 SQ Sequence 331 AA;
 Query Match 100.0%; Score 85; DB 3; Length 331;
 Best Local Similarity 100.0%; Pred. No. 1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HSSDYSWVRKNQYVS 15
 Db |||||
 77 HSSDYSWVRKNQYVS 91
 RESULT 14
 AAM93324
 ID AAM93324 standard; protein; 331 AA.
 AC
 XX AAM93324;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human polypeptide, SEQ ID NO: 2847.
 XX
 DE Human; full length cDNA; cDNA synthesis; oligo-capping.
 KW
 XX Homo sapiens.
 OS
 XX EP1130094-A2.
 PN
 XX 05-SEP-2001.
 PD
 XX 07-JUL-2000; 2000EP-00114089.
 PF
 XX 08-JUL-1999; 99JP-00194486.
 PR
 PR 11-JAN-2000; 2000JP-00118774.
 PR
 XX 02-MAY-2000; 2000JP-00183765.
 XX
 PA (HELI-) HELIX RES INST.
 XX
 XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
 XX
 XX WPI: 2001-524255/58.
 DR N-PSDB; AAK94244.
 DR
 XX
 XX 830 Primers useful for synthesizing full length cDNA clones and their use
 PT in genetic manipulation.
 PS Claim 8; SEQ ID NO 2847; 1380pp + Sequence Listing; English.
 XX
 CC The invention relates to primers for synthesizing full length cDNA
 CC clones. 830 cDNA molecules encoding a human protein have been isolated
 CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
 CC been determined. Primers for synthesizing the full length cDNA are useful
 CC for clarifying the function of the protein encoded by the cDNA. The full
 CC length clones were obtained by construction of full length enriched cDNA
 CC libraries that were synthesised by the oligo-capping method. The primers
 CC enable the production of the full length cDNA easily without any special
 CC methods. The present sequence is a polypeptide encoded by a full length
 CC human cDNA of the invention. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in CD-ROM
 CC format directly from EPO
 XX
 SQ Sequence 331 AA;

CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
 CC been determined. Primers for synthesizing the full length cDNA are useful
 CC for clarifying the function of the protein encoded by the cDNA. The full
 CC length clones were obtained by construction of full length enriched cDNA
 CC libraries that were synthesised by the oligo-capping method. The primers
 CC enable the production of the full length cDNA easily without any special
 CC methods. The present sequence is a polypeptide encoded by a full length
 CC human cDNA of the invention. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in CD-ROM
 CC format directly from EPO
 XX
 SQ Sequence 331 AA;
 Query Match 100.0%; Score 85; DB 4; Length 331;
 Best Local Similarity 100.0%; Pred. No. 1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HSSDYSWVRKNQYVS 15
 Db |||||
 77 HSSDYSWVRKNQYVS 91
 RESULT 14
 AAM93324
 ID AAM93324 standard; protein; 331 AA.
 AC
 XX AAM93324;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human polypeptide, SEQ ID NO: 2847.
 XX
 DE Human; full length cDNA; cDNA synthesis; oligo-capping.
 KW
 XX Homo sapiens.
 OS
 XX EP1130094-A2.
 PN
 XX 05-SEP-2001.
 PD
 XX 07-JUL-2000; 2000EP-00114089.
 PF
 XX 08-JUL-1999; 99JP-00194486.
 PR
 PR 11-JAN-2000; 2000JP-00118774.
 PR
 XX 02-MAY-2000; 2000JP-00183765.
 XX
 PA (HELI-) HELIX RES INST.
 XX
 XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
 XX
 XX WPI: 2001-524255/58.
 DR N-PSDB; AAK94244.
 DR
 XX
 XX 830 Primers useful for synthesizing full length cDNA clones and their use
 PT in genetic manipulation.
 PS Claim 8; SEQ ID NO 2847; 1380pp + Sequence Listing; English.
 XX
 CC The invention relates to primers for synthesizing full length cDNA
 CC clones. 830 cDNA molecules encoding a human protein have been isolated
 CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
 CC been determined. Primers for synthesizing the full length cDNA are useful
 CC for clarifying the function of the protein encoded by the cDNA. The full
 CC length clones were obtained by construction of full length enriched cDNA
 CC libraries that were synthesised by the oligo-capping method. The primers
 CC enable the production of the full length cDNA easily without any special
 CC methods. The present sequence is a polypeptide encoded by a full length
 CC human cDNA of the invention. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in CD-ROM
 CC format directly from EPO
 XX
 SQ Sequence 331 AA;

Query Match 100.0%; Score 85; DB 4; Length 331;
 Best Local Similarity 100.0%; Pred. No. 1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSSDYSNMRKNQYVS 15
 |||||
 DB 77 HSSDYSNMRKNQYVS 91

RESULT 15
 AAM38872
 ID AAM38872 standard; protein; 331 AA.
 XX AC AAM38872;
 XX DT 22-OCT-2001 (first entry)
 XX DE Human polypeptide SEQ ID NO 2017.
 XX KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.
 XX OS Homo sapiens.
 XX PN WO200153312-A1.
 XX PD 26-JUL-2001.
 XX PF 26-DEC-2000; 2000WO-US034263.
 XX PR 23-DEC-1999; 99US-00471275.
 PR 21-JAN-2000; 2000US-00488725.
 PR 25-APR-2000; 2000US-00552317.
 PR 20-JUN-2000; 2000US-00598042.
 PR 19-JUL-2000; 2000US-00620312.
 PR 03-AUG-2000; 2000US-00653450.
 PR 14-SEP-2000; 2000US-00662191.
 PR 19-OCT-2000; 2000US-00693036.
 PR 29-NOV-2000; 2000US-00727344.
 XX PA (HYSE-) HYSEQ INC.
 XX PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
 PI Zhou P, Goodrich R, Drmanac RT;
 XX WPI; 2001-442253/47.
 DR N-PSDB; AAI58028.
 XX PT Novel nucleic acids and polypeptides, useful for treating disorders such
 PT as central nervous system injuries.
 XX PS Example 3; SEQ ID NO 2017; 10078pp; English.
 XX CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the
 CC encoded polypeptides (AAM38642-AAM42213) with nootropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders. Note: The sequence data for this patent did not form

CC part of the printed specification
 XX SQ Sequence 331 AA;
 Query Match 100.0%; Score 85; DB 4; Length 331;
 Best Local Similarity 100.0%; Pred. No. 1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSSDYSNMRKNQYVS 15
 |||||
 DB 77 HSSDYSNMRKNQYVS 91

Search completed: June 3, 2005, 08:21:44
 Job time : 16.825 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 3, 2005, 08:28:22 ; Search time 12.15 Seconds
(without alignments)
426.765 Million cell updates/sec

Title: US-10-616-279-10

Perfect score: 85

Sequence: 1 HSSDYSWVRKNQYVS 15

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1465611 seqs, 345679903 residues

Total number of hits satisfying chosen parameters: 1465611

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_5/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	100.0	15	9	US-09-732-357A-10
2	85	100.0	15	15	US-10-616-279-10
3	85	100.0	15	16	US-10-624-884-10
4	85	100.0	15	17	US-10-895-183-10
5	85	100.0	290	15	US-10-629-952-4
6	85	100.0	330	9	US-09-903-383-2
7	85	100.0	331	9	US-09-732-357A-2
8	85	100.0	331	9	US-09-978-295A-236
9	85	100.0	331	9	US-09-938-418-8
10	85	100.0	331	9	US-09-978-697-236
11	85	100.0	331	9	US-09-978-192A-236
12	85	100.0	331	9	US-09-999-832A-236
13	85	100.0	331	10	US-09-978-189-236

14	85	100.0	331	10	US-09-978-608A-236	Sequence 236, App
15	85	100.0	331	10	US-09-978-585A-236	Sequence 236, App
16	85	100.0	331	10	US-09-978-191A-236	Sequence 236, App
17	85	100.0	331	10	US-09-978-403A-236	Sequence 236, App
18	85	100.0	331	10	US-09-978-564A-236	Sequence 236, App
19	85	100.0	331	10	US-09-999-833A-236	Sequence 236, App
20	85	100.0	331	10	US-09-981-915A-236	Sequence 236, App
21	85	100.0	331	10	US-09-978-824-236	Sequence 236, App
22	85	100.0	331	10	US-09-918-585A-236	Sequence 236, App
23	85	100.0	331	10	US-09-999-834A-236	Sequence 236, App
24	85	100.0	331	10	US-09-978-423A-236	Sequence 236, App
25	85	100.0	331	10	US-09-978-193A-236	Sequence 236, App
26	85	100.0	331	10	US-09-999-830A-236	Sequence 236, App
27	85	100.0	331	10	US-09-978-757A-236	Sequence 236, App
28	85	100.0	331	10	US-09-978-187B-236	Sequence 236, App
29	85	100.0	331	10	US-09-978-643A-236	Sequence 236, App
30	85	100.0	331	10	US-09-978-375A-236	Sequence 236, App
31	85	100.0	331	10	US-09-978-298A-236	Sequence 236, App
32	85	100.0	331	10	US-09-978-188A-236	Sequence 236, App
33	85	100.0	331	10	US-09-978-681A-236	Sequence 236, App
34	85	100.0	331	10	US-09-978-194A-236	Sequence 236, App
35	85	100.0	331	10	US-09-999-829A-236	Sequence 236, App
36	85	100.0	331	10	US-09-978-299A-236	Sequence 236, App
37	85	100.0	331	10	US-09-978-544A-236	Sequence 236, App
38	85	100.0	331	10	US-09-978-665A-236	Sequence 236, App
39	85	100.0	331	10	US-09-978-802A-236	Sequence 236, App
40	85	100.0	331	10	US-09-970-944-12	Sequence 12, Appl
41	85	100.0	331	10	US-09-970-944-39	Sequence 39, Appl
42	85	100.0	331	10	US-09-970-944-40	Sequence 40, Appl
43	85	100.0	331	11	US-09-999-831A-236	Sequence 236, App
44	85	100.0	331	14	US-10-017-081A-236	Sequence 236, App
45	85	100.0	331	14	US-10-017-081A-236	Sequence 236, App

ALIGNMENTS

RESULT 1
US-09-732-357A-10
; Sequence 10, Application US/09732357A
; Patent No. US20020004047A1
; GENERAL INFORMATION:
; APPLICANT: Harkins, Richard
; APPLICANT: Parkes, Deborah
; APPLICANT: Parry, Gordon
; APPLICANT: Schneider, Douglas
; APPLICANT: Steinbrecher, Renate
; TITLE OF INVENTION: DNA Encoding a No. US20020004047A1el RG-1 Polypeptide
; FILE REFERENCE: 51791AUSM1
; CURRENT APPLICATION NUMBER: US/09732,357A
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/172,370
; PRIOR FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-732-357A-10

Query Match 100.0%; Score 85; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSSDYSWVRKNQYVS 15

Db 1 HSSDYSWVRKNQYVS 15

RESULT 2

US-10-616-279-10

; Sequence 10, Application US/10616279

```
; Publication No. US20040023307A1
; GENERAL INFORMATION:
; APPLICANT: Harkins, Richard
; APPLICANT: Parkes, Deborah
; APPLICANT: Parry, Gordon
; APPLICANT: Schneider, Douglas
; TITLE OF INVENTION: DNA Encoding a No. US20040023307A1el RG-1 Polypeptide
; FILE REFERENCE: 51791AUSD1
; CURRENT APPLICATION NUMBER: US/10/616,279
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: US 60/172,370
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: US 09/732,357
; PRIOR FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-616-279-10

Query Match      100.0%; Score 85; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSSDYSWMRKNOYVS 15
Db 1 HSSDYSWMRKNOYVS 15

RESULT 3
US-10-624-884-10
; Sequence 10, Application US/10624884
; Publication No. US20040152139A1
; GENERAL INFORMATION:
; APPLICANT: Harkins, Richard
; APPLICANT: Parkes, Deborah
; APPLICANT: Parry, Gordon
; APPLICANT: Schneider, Douglas
; APPLICANT: Steinbrecher, Renate
; TITLE OF INVENTION: DNA Encoding a Novel RG-1 Polypeptide
; FILE REFERENCE: 51791AUSC1
; CURRENT APPLICATION NUMBER: US/10/624,884
; CURRENT FILING DATE: 2003-07-22
; PRIOR APPLICATION NUMBER: US 60/172,370
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: US 09/732,357
; PRIOR FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-624-884-10

Query Match      100.0%; Score 85; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSSDYSWMRKNOYVS 15
Db 1 HSSDYSWMRKNOYVS 15

RESULT 4
US-10-895-183-10
; Sequence 10, Application US/10895183
; Publication No. US20050019845A1
; GENERAL INFORMATION:
; APPLICANT: Harkins, Richard
```

```
; APPLICANT: Parkes, Deborah
; APPLICANT: Parry, Gordon
; APPLICANT: Schneider, Douglas
; APPLICANT: Steinbrecher, Renate
; TITLE OF INVENTION: Rg1 Antibodies and Uses Thereof
; FILE REFERENCE: 51791BUSM1
; CURRENT APPLICATION NUMBER: US/10/895,183
; CURRENT FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: US 60/489,032
; PRIOR FILING DATE: 2003-07-22
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-895-183-10

Query Match      100.0%; Score 85; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSSDYSWMRKNOYVS 15
Db 1 HSSDYSWMRKNOYVS 15

RESULT 5
US-10-629-952-4
; Sequence 4, Application US/10629952
; Publication No. US20040072227A1
; GENERAL INFORMATION:
; APPLICANT: Jonak, Zdenka L
; APPLICANT: Trullii, Stephen H
; APPLICANT: Tsui, Ping
; APPLICANT: Lane, Pamela A.
; TITLE OF INVENTION: INTEGRIN LIGAND, HUMAN MINDIN
; FILE REFERENCE: DDX-100US
; CURRENT APPLICATION NUMBER: US/10/629,952
; CURRENT FILING DATE: 2003-07-29
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 290
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-10-629-952-4

Query Match      100.0%; Score 85; DB 15; Length 290;
Best Local Similarity 100.0%; Pred. No. 7.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSSDYSWMRKNOYVS 15
Db 77 HSSDYSWMRKNOYVS 91

RESULT 6
US-09-903-383-2
; Sequence 2, Application US/09903383
; Patent No. US20020137135A1
; GENERAL INFORMATION:
; APPLICANT: Sytkowski, Arthur J.
; APPLICANT: Yang, Meiheng
; TITLE OF INVENTION: NOVEL NFG-1 GENE THAT IS DIFFERENTIALLY EXPRESSED IN PROSTATE
; FILE REFERENCE: 01948/053002
; CURRENT APPLICATION NUMBER: US/09/903,383
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/371,696
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 09/022,238
; PRIOR FILING DATE: 1998-02-11
```

; PRIOR APPLICATION NUMBER: US 08/644,326
; PRIOR FILING DATE: 1996-05-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-903-383-2

Query Match 100.0%; Score 85; DB 9; Length 330;
Best Local Similarity 100.0%; Pred. No. 8.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSSDYSWMRKQYVS 15
Db 77 HSSDYSWMRKQYVS 91
|||||

RESULT 7
US-09-732-357A-2
; Sequence 2, Application US/09732357A
; Patent No. US20020004047A1
; GENERAL INFORMATION:
; APPLICANT: Harkins, Richard
; APPLICANT: Parkes, Deborah
; APPLICANT: Parry, Gordon
; APPLICANT: Schneider, Douglas
; APPLICANT: Steinbrecher, Renate
; TITLE OF INVENTION: DNA Encoding a No. US20020004047A1el RG-1 Polypeptide
; FILE REFERENCE: 51791AUSM1
; CURRENT APPLICATION NUMBER: US/09/732,357A
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/172,370
; PRIOR FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-732-357A-2

Query Match 100.0%; Score 85; DB 9; Length 331;
Best Local Similarity 100.0%; Pred. No. 8.7e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSSDYSWMRKQYVS 15
Db 77 HSSDYSWMRKQYVS 91
|||||

RESULT 8
US-09-978-295A-236
; Sequence 236, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C11
; CURRENT APPLICATION NUMBER: US/09/978,295A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078004
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079663
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079786
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079920
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/079923
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/080105
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080165
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327

; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080328
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080334
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081070
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081071
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081203
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081229
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081817
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081952
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081838
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082569
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082700
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082796
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: 60/083336
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/083392
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083495
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083496
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083499
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083545
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083554
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083558
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083559
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083500
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083742
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: 60/084366
; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06

; PRIOR APPLICATION NUMBER: 60/084637
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084598
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084627
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 85; DB 9; Length 331;
Best Local Similarity 100.0%; Pred. No. 8.7e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSSDYSMWRKNQYVS 15
Db 77 HSSDYSMWRKNQYVS 91

RESULT 9
US-09-938-418-8
; Sequence 8, Application US/09938418
; Patent No. US20020161199A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Gurney, Austin L.
; APPLICANT: Polakis, Paul
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Wu, Thomas D.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5009R1
; CURRENT APPLICATION NUMBER: US/09/938,418
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: 60/081,071
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: 60/085,697
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/097,022
; PRIOR FILING DATE: 1998-08-18
; PRIOR APPLICATION NUMBER: 60/101,922
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/103,679

;; PRIOR FILING DATE: 1998-10-08
;; PRIOR APPLICATION NUMBER: PCT/US99/05028
;; PRIOR FILING DATE: 1999-03-08
;; PRIOR APPLICATION NUMBER: PCT/US99/12252
;; PRIOR FILING DATE: 1999-06-02
;; PRIOR APPLICATION NUMBER: PCT/US99/20111
;; PRIOR FILING DATE: 1999-09-01
;; PRIOR APPLICATION NUMBER: PCT/US99/28565
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US00/04342
;; PRIOR FILING DATE: 2000-02-18
;; PRIOR APPLICATION NUMBER: PCT/US00/04341
;; PRIOR FILING DATE: 2000-02-18
;; PRIOR APPLICATION NUMBER: PCT/US00/05841
;; PRIOR FILING DATE: 2000-03-02
;; PRIOR APPLICATION NUMBER: PCT/US00/08439
;; PRIOR FILING DATE: 2000-03-30
;; PRIOR APPLICATION NUMBER: PCT/US00/14042
;; PRIOR FILING DATE: 2000-05-22
;; PRIOR APPLICATION NUMBER: PCT/US00/23328
;; PRIOR FILING DATE: 2000-08-24
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: 2000-12-01
;; PRIOR APPLICATION NUMBER: PCT/US01/06520
;; PRIOR FILING DATE: 2001-02-28
;; PRIOR APPLICATION NUMBER: PCT/US01/17800
;; PRIOR FILING DATE: 2001-06-01
;; PRIOR APPLICATION NUMBER: PCT/US01/19692
;; PRIOR FILING DATE: 2001-06-20
;; PRIOR APPLICATION NUMBER: PCT/US01/21066
;; PRIOR FILING DATE: 2001-06-29
;; PRIOR APPLICATION NUMBER: PCT/US01/21735
;; PRIOR FILING DATE: 2001-07-09
;; NUMBER OF SEQ ID NOS: 10
;; SEQ ID NO 8
;; LENGTH: 331
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-938-418-8

Query Match 100.0%; Score 85; DB 9; Length 331;
Best Local Similarity 100.0%; Pred. No. 8.7e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 HSSDYSWNRKNQYVS 15
Db 77 HSSDYSWNRKNQYVS 91
|||||

RESULT 10
US-09-978-697-236
; Sequence 236, Application US/09978697
; Patent No. US20020169284A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.

;; APPLICANT: Pan, James;
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Shelton, David L.
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2630P1C27
;; CURRENT APPLICATION NUMBER: US/09/978.697
;; CURRENT FILING DATE: 2001-10-16
;; PRIOR APPLICATION NUMBER: 05/918585
;; PRIOR FILING DATE: 2001-07-30
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/064249
;; PRIOR FILING DATE: 1997-11-03
;; PRIOR APPLICATION NUMBER: 60/065311
;; PRIOR FILING DATE: 1997-11-13
;; PRIOR APPLICATION NUMBER: 60/066364
;; PRIOR FILING DATE: 1997-11-21
;; PRIOR APPLICATION NUMBER: 60/077450
;; PRIOR FILING DATE: 1998-03-10
;; PRIOR APPLICATION NUMBER: 60/077632
;; PRIOR FILING DATE: 1998-03-11
;; PRIOR APPLICATION NUMBER: 60/077641
;; PRIOR FILING DATE: 1998-03-11
;; PRIOR APPLICATION NUMBER: 60/077649
;; PRIOR FILING DATE: 1998-03-11
;; PRIOR APPLICATION NUMBER: 60/077791
;; PRIOR FILING DATE: 1998-03-12
;; PRIOR APPLICATION NUMBER: 60/078004
;; PRIOR FILING DATE: 1998-03-13
;; PRIOR APPLICATION NUMBER: 60/078886
;; PRIOR FILING DATE: 1998-03-20
;; PRIOR APPLICATION NUMBER: 60/078936
;; PRIOR FILING DATE: 1998-03-20
;; PRIOR APPLICATION NUMBER: 60/078910
;; PRIOR FILING DATE: 1998-03-20
;; PRIOR APPLICATION NUMBER: 60/078939
;; PRIOR FILING DATE: 1998-03-20
;; PRIOR APPLICATION NUMBER: 60/079294
;; PRIOR FILING DATE: 1998-03-25
;; PRIOR APPLICATION NUMBER: 60/079656
;; PRIOR FILING DATE: 1998-03-26
;; PRIOR APPLICATION NUMBER: 60/079664
;; PRIOR FILING DATE: 1998-03-27
;; PRIOR APPLICATION NUMBER: 60/079689
;; PRIOR FILING DATE: 1998-03-27
;; PRIOR APPLICATION NUMBER: 60/079663
;; PRIOR FILING DATE: 1998-03-27
;; PRIOR APPLICATION NUMBER: 60/079728
;; PRIOR FILING DATE: 1998-03-27
;; PRIOR APPLICATION NUMBER: 60/079786
;; PRIOR FILING DATE: 1998-03-27
;; PRIOR APPLICATION NUMBER: 60/079920
;; PRIOR FILING DATE: 1998-03-30
;; PRIOR APPLICATION NUMBER: 60/079923
;; PRIOR FILING DATE: 1998-03-30
;; PRIOR APPLICATION NUMBER: 60/080105
;; PRIOR FILING DATE: 1998-03-31
;; PRIOR APPLICATION NUMBER: 60/080107
;; PRIOR FILING DATE: 1998-03-31
;; PRIOR APPLICATION NUMBER: 60/080165
;; PRIOR FILING DATE: 1998-03-31
;; PRIOR APPLICATION NUMBER: 60/080194
;; PRIOR FILING DATE: 1998-03-31
;; PRIOR APPLICATION NUMBER: 60/080327
;; PRIOR FILING DATE: 1998-04-01
;; PRIOR APPLICATION NUMBER: 60/080328
;; PRIOR FILING DATE: 1998-04-01

```

; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080334
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081070
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081071
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081203
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081229
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081817
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081952
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081838
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082569
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082700
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082796
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: 60/083336
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/083392
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083495
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083496
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083499
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083545
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083554
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083558
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083559
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083500
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083742
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: 60/084366
; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084637
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084639

```

```

; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084598
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-5-07
; PRIOR APPLICATION NUMBER: 60/084627
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

```

Query Match 100.0%; Score 85; DB 9; Length 331;
 Best Local Similarity 100.0%; Pred. No. 8.7e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 15; Conservative 0;

```

Qy 1 HSSDYSMWRKNQYVS 15
    |||||
Db 77 HSSDYSMWRKNQYVS 91

```

```

RESULT 11
US-09-978-192A-236
; Sequence 236, Application US/09978192A
; Patent No. US20020177553A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey

```

```

; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC9
; CURRENT APPLICATION NUMBER: US/09/378,192A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078004
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079663
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079786
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079920
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/079923
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/080105
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080165
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080328
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080334
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081070
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081071
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081203
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081229
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081817
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081952
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081838
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082569
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082700
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082796
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: 60/083336
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/083392
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083495
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083496
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083499
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083545
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083554
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083558
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083559
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083500
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083742
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: 60/084366
; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084637
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084598
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07

```

```

; PRIOR APPLICATION NUMBER: 60/084627
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

```

Query Match 100.0%; Score 85; DB 9; Length 331;

Best Local Similarity 100.0%; Pred. No. 8.7e-05; Mismatches 0; Indels 0; Gaps 0;

```

Matches 15; Conservative 0;
QY 1 HSSDYSMRKNQYVS 15
Db 77 HSSDYSMRKNQYVS 91

```

RESULT 12

US-09-999-832A-236

Sequence 236, Application US/09999832A

Publication No. US20020192706A1

GENERAL INFORMATION:

```

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C63
; CURRENT APPLICATION NUMBER: US/09/999,832A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585

```

```

; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078004
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079663
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079786
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079920
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/079923
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/080105
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080165
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080328
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080334
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081070
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081071
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081203
; PRIOR FILING DATE: 1998-04-09

```


; PRIOR APPLICATION NUMBER: 60/081229
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081817
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081952
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081838
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082569
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082700
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082796
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: 60/083336
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/083392
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083495
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083496
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083499
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083545
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083554
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083558
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083559
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083500
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083742
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: 60/084366
; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084637
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084598
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084627
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338

; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 85; DB 9; Length 331;
Best Local Similarity 100.0%; Pred. No. 8.7e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSSDYSMRKNQYVS 15
Db 77 HSSDYSMRKNQYVS 91
|||||

RESULT 13

US-09-978-189-236
; Sequence 236, Application US/09978189
; Publication No. US20030004102A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C7
; CURRENT APPLICATION NUMBER: US/09/978,189
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13

1	PRIOR FILING DATE: 1998-04-15	
2	PRIOR APPLICATION NUMBER: 60/081952	
3	PRIOR FILING DATE: 1998-04-15	
4	PRIOR APPLICATION NUMBER: 60/081838	
5	PRIOR FILING DATE: 1998-04-15	
6	PRIOR APPLICATION NUMBER: 60/082568	
7	PRIOR FILING DATE: 1998-04-21	
8	PRIOR APPLICATION NUMBER: 60/082569	
9	PRIOR FILING DATE: 1998-04-21	
10	PRIOR APPLICATION NUMBER: 60/082704	
11	PRIOR FILING DATE: 1998-04-22	
12	PRIOR APPLICATION NUMBER: 60/082804	
13	PRIOR FILING DATE: 1998-04-22	
14	PRIOR APPLICATION NUMBER: 60/082700	
15	PRIOR FILING DATE: 1998-04-22	
16	PRIOR APPLICATION NUMBER: 60/082797	
17	PRIOR FILING DATE: 1998-04-22	
18	PRIOR APPLICATION NUMBER: 60/082796	
19	PRIOR FILING DATE: 1998-04-23	
20	PRIOR APPLICATION NUMBER: 60/083336	
21	PRIOR FILING DATE: 1998-04-27	
22	PRIOR APPLICATION NUMBER: 60/083322	
23	PRIOR FILING DATE: 1998-04-28	
24	PRIOR APPLICATION NUMBER: 60/083392	
25	PRIOR FILING DATE: 1998-04-29	
26	PRIOR APPLICATION NUMBER: 60/083495	
27	PRIOR FILING DATE: 1998-04-29	
28	PRIOR APPLICATION NUMBER: 60/083496	
29	PRIOR FILING DATE: 1998-04-29	
30	PRIOR APPLICATION NUMBER: 60/083499	
31	PRIOR FILING DATE: 1998-04-29	
32	PRIOR APPLICATION NUMBER: 60/083545	
33	PRIOR FILING DATE: 1998-04-29	
34	PRIOR APPLICATION NUMBER: 60/083554	
35	PRIOR FILING DATE: 1998-04-29	
36	PRIOR APPLICATION NUMBER: 60/083558	
37	PRIOR FILING DATE: 1998-04-29	
38	PRIOR APPLICATION NUMBER: 60/083559	
39	PRIOR FILING DATE: 1998-04-29	
40	PRIOR APPLICATION NUMBER: 60/083500	
41	PRIOR FILING DATE: 1998-04-29	
42	PRIOR APPLICATION NUMBER: 60/083742	
43	PRIOR FILING DATE: 1998-04-30	
44	PRIOR APPLICATION NUMBER: 60/084366	
45	PRIOR FILING DATE: 1998-05-05	
46	PRIOR APPLICATION NUMBER: 60/084414	
47	PRIOR FILING DATE: 1998-05-06	
48	PRIOR APPLICATION NUMBER: 60/084441	
49	PRIOR FILING DATE: 1998-05-06	
50	PRIOR APPLICATION NUMBER: 60/084637	
51	PRIOR FILING DATE: 1998-05-07	
52	PRIOR APPLICATION NUMBER: 60/084639	
53	PRIOR FILING DATE: 1998-05-07	
54	PRIOR APPLICATION NUMBER: 60/084640	
55	PRIOR FILING DATE: 1998-05-07	
56	PRIOR APPLICATION NUMBER: 60/084598	
57	PRIOR FILING DATE: 1998-05-07	
58	PRIOR APPLICATION NUMBER: 60/084600	
59	PRIOR FILING DATE: 1998-5-07	
60	PRIOR APPLICATION NUMBER: 60/084627	
61	PRIOR FILING DATE: 1998-05-07	
62	PRIOR APPLICATION NUMBER: 60/084643	
63	PRIOR FILING DATE: 1998-05-07	
64	PRIOR APPLICATION NUMBER: 60/085339	
65	PRIOR FILING DATE: 1998-05-13	
66	PRIOR APPLICATION NUMBER: 60/085338	
67	PRIOR FILING DATE: 1998-05-13	
68	PRIOR APPLICATION NUMBER: 60/085323	
69	PRIOR FILING DATE: 1998-05-13	
70	PRIOR APPLICATION NUMBER: 60/085582	
71	PRIOR FILING DATE: 1998-05-15	
72	PRIOR APPLICATION NUMBER: 60/085700	
73	PRIOR FILING DATE: 1998-05-15	

```

RESULT 15
US-09-978-585A-236
; Sequence 236, Application US/09978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC15
; CURRENT APPLICATION NUMBER: US/09/978,585A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior application removed - See File Wrapper or Palm
; SEQ ID NO 236
; LENGTH: 331
; TYPE: PrT
; ORGANISM: Homo sapiens
US-09-978-585A-236

Query Match      100.0%; Score 85; DB 10; Length 331;
Best Local Similarity 100.0%; Pred.No. 8.7e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps

QY   1 HSSDYSMMRKNOYVS 15
Db    77 HSSDYSMMRKNOYVS 91
                                     |||||
Search completed: June 3, 2005, 09:01:04
Job time : 13.35 secs
```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 3, 2005, 08:10:06 ; Search time 4.1625 Seconds
(without alignments)
269.006 Million cell updates/sec

Title: US-10-616-279-10

Perfect score: 85

Sequence: 1 HSSDYSWNRKNQVVS 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	100.0	15	4	US-09-732-357B-10
2	85	100.0	330	3	US-09-371-696-2
3	85	100.0	331	2	US-08-799-173A-2
4	85	100.0	331	4	US-09-732-357B-2
5	85	100.0	331	4	US-09-170-042A-2
6	82	96.5	330	4	US-09-732-357B-13
7	52	61.2	299	4	US-09-311-021-202
8	44	51.8	677	4	US-09-270-767-58094
9	44	51.8	847	4	US-09-270-767-42783
10	42	49.4	25	4	US-09-270-767-58735
11	42	49.4	250	4	US-09-248-796A-15562
12	42	49.4	435	3	US-09-072-917A-9
13	42	49.4	877	4	US-09-165-396-5
14	41	48.2	149	4	US-09-270-767-47885
15	41	48.2	297	4	US-09-248-796A-25364
16	40	47.1	111	4	US-09-248-796A-21330
17	40	47.1	114	4	US-09-513-999C-5768
18	40	47.1	456	4	US-09-489-039A-8101
19	40	47.1	462	4	US-09-543-681A-5290
20	40	47.1	742	4	US-09-500-123-12
21	40	47.1	811	4	US-09-500-123-9
22	40	47.1	871	4	US-09-500-123-7
23	40	47.1	1008	4	US-09-949-016-10423
24	39	45.9	152	4	US-09-270-767-37205
25	39	45.9	152	4	US-09-270-767-52422
26	39	45.9	163	4	US-09-328-352-7800
27	39	45.9	249	4	US-09-270-767-43254

28	39	45.9	281	4	US-09-248-796A-23359	Sequence 23359, A
29	39	45.9	635	4	US-09-248-796A-16944	Sequence 16944, A
30	39	45.9	1085	1	US-08-431-080-28	Sequence 28, Appl
31	39	45.9	1085	2	US-08-938-534-28	Sequence 28, Appl
32	39	45.9	1085	3	US-09-345-294-28	Sequence 28, Appl
33	39	45.9	1169	1	US-08-542-921-2	Sequence 2, Appl
34	39	45.9	1169	2	US-08-880-685-2	Sequence 2, Appl
35	39	45.9	1169	2	US-08-880-684-2	Sequence 2, Appl
36	38.5	45.3	404	4	US-09-248-796A-19544	Sequence 19544, A
37	38	44.7	126	4	US-09-755-665-27	Sequence 27, Appl
38	38	44.7	133	4	US-09-755-665-4	Sequence 4, Appl
39	38	44.7	172	4	US-08-737-109-17	Sequence 17, Appl
40	38	44.7	185	4	US-09-248-796A-14213	Sequence 14213, A
41	38	44.7	319	4	US-09-107-532A-6215	Sequence 6215, Ap
42	38	44.7	321	3	US-08-915-795-9	Sequence 9, Appl
43	38	44.7	321	4	US-09-847-524-4	Sequence 4, Appl
44	38	44.7	321	4	US-09-296-275-9	Sequence 9, Appl
45	38	44.7	325	3	US-08-915-795-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-09-732-357B-10
; Sequence 10, Application US/09732357B
; Patent No. 6682902
; GENERAL INFORMATION:
; APPLICANT: Harkins, Richard
; APPLICANT: Parkes, Deborah
; APPLICANT: Parry, Gordon
; APPLICANT: Schneider, Douglas
; APPLICANT: Steinbrecher, Renate
; TITLE OF INVENTION: DNA Encoding a No. 6682902el RG-1 Polypeptide
; FILE REFERENCE: 51791AUSM1
; CURRENT APPLICATION NUMBER: US/09732,357B
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/172,370
; PRIOR FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-732-357B-10

Query Match 100.0%; Score 85; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSSDYSWNRKNQVVS 15
| | | | | | | | | | | | | | |
DB 1 HSSDYSWNRKNQVVS 15

RESULT 2
US-09-371-696-2
; Sequence 2, Application US/09371696
; Patent No. 628777
; GENERAL INFORMATION:
; APPLICANT: Sytkowski, Arthur J.
; APPLICANT: Yang, Meiheng
; TITLE OF INVENTION: NOVEL NPG-1 GENE THAT IS DIFFERENTIALLY EXPRESSED IN PROSTATE
; FILE REFERENCE: 01948/053002
; CURRENT APPLICATION NUMBER: US/09371,696
; CURRENT FILING DATE: 1999-08-10
; EARLIER APPLICATION NUMBER: US 09/022,238
; EARLIER FILING DATE: 1998-02-11
; EARLIER APPLICATION NUMBER: US 08/644,326
; EARLIER FILING DATE: 1996-05-10
; NUMBER OF SEQ ID NOS: 5

```
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-371-696-2

Query Match      100.0%; Score 85; DB 3; Length 330;
Best Local Similarity 100.0%; Pred. No. 4.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSSDYSWVRKNQYVS 15
   |||||
Db 77 HSSDYSWVRKNQYVS 91

RESULT 3
US-08-799-173A-2
; Sequence 2, Application US/08799173A
; Patent No. 5871969
; GENERAL INFORMATION:
; APPLICANT: HASTINGS, GREGG.
; APPLICANT: PATRICK J. DILLON
; TITLE OF INVENTION: HUMAN NEURONAL ATTACHMENT FACTOR-1
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/799,173A
; FILING DATE: 11-FEB-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF226
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 331 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-799-173A-2

Query Match      100.0%; Score 85; DB 2; Length 331;
Best Local Similarity 100.0%; Pred. No. 4.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSSDYSWVRKNQYVS 15
   |||||
Db 77 HSSDYSWVRKNQYVS 91

RESULT 4
US-09-732-357B-2
; Sequence 2, Application US/09732357B
; Patent No. 6682902
; GENERAL INFORMATION:
; APPLICANT: Harkins, Richard
; APPLICANT: Parkes, Deborah
; APPLICANT: Parry, Gordon
; TITLE OF INVENTION: DNA Encoding a No. 6682902el RG-1 Polypeptide
; FILE REFERENCE: 51791AUSM1
; CURRENT APPLICATION NUMBER: US/09/732,357B
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/172,370
; PRIOR FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 13
; LENGTH: 330
; ORGANISM: Homo sapiens
US-09-732-357B-2

Query Match      100.0%; Score 85; DB 4; Length 331;
Best Local Similarity 100.0%; Pred. No. 4.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSSDYSWVRKNQYVS 15
   |||||
Db 77 HSSDYSWVRKNQYVS 91

RESULT 5
US-09-170-042A-2
; Sequence 2, Application US/09170042A
; Patent No. 6759512
; GENERAL INFORMATION:
; APPLICANT: Hastings, Gregg
; APPLICANT: Dillon, Patrick
; TITLE OF INVENTION: Human Neuronal Attachment Factor-1
; FILE REFERENCE: PF226D1
; CURRENT APPLICATION NUMBER: US/09/170,042A
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2
; LENGTH: 331
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-170-042A-2

Query Match      100.0%; Score 85; DB 4; Length 331;
Best Local Similarity 100.0%; Pred. No. 4.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HSSDYSWVRKNQYVS 15
   |||||
Db 77 HSSDYSWVRKNQYVS 91

RESULT 6
US-09-732-357B-13
; Sequence 13, Application US/09732357B
; Patent No. 6682902
; GENERAL INFORMATION:
; APPLICANT: Harkins, Richard
; APPLICANT: Parkes, Deborah
; APPLICANT: Parry, Gordon
; APPLICANT: Schneider, Douglas
; APPLICANT: Steinbrecher, Renate
; TITLE OF INVENTION: DNA Encoding a No. 6682902el RG-1 Polypeptide
; FILE REFERENCE: 51791AUSM1
; CURRENT APPLICATION NUMBER: US/09/732,357B
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/172,370
; PRIOR FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 13
; LENGTH: 330
; ORGANISM: Homo sapiens
US-09-732-357B-13
```

```
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-732-357B-13

Query Match      96.5%; Score 82; DB 4; Length 330;
Best Local Similarity 93.3%; Pred. No. 1.4e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSSDYSMRKNQYVS 15
Db 76 HSSDYSMRKNQYVS 90
|||||:|||||

RESULT 7
US-09-311-021-202
; Sequence 202, Application US/09311021
; Patent No. 6706869
; GENERAL INFORMATION:
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fachtel, Kim
; APPLICANT: Agostino, Michael J.
; TITLE OF INVENTION: GENETICS INSTITUTE, INC.
; FILE REFERENCE: GI 6300-11A
; CURRENT APPLICATION NUMBER: US/09/311.021
; CURRENT FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 202
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-311-021-202

Query Match      61.2%; Score 52; DB 4; Length 299;
Best Local Similarity 100.0%; Pred. No. 0.89;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MWRKNQYVS 15
Db 1 MWRKNQYVS 9
|||||:|||||

RESULT 8
US-09-270-767-58094
; Sequence 58094, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58094
; LENGTH: 677
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-58094

Query Match      51.8%; Score 44; DB 4; Length 677;
Best Local Similarity 46.7%; Pred. No. 41;
Matches 7; Conservative 1; Mismatches 7; Indels 7; Gaps 0;

Qy 1 HSSDYSMRKNQYVS 15
Db 230 HSSDYRFWESGELAS 244
|||||:|:|

RESULT 9
US-09-270-767-42783
```

```
; Sequence 42783, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42783
; LENGTH: 847
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-42783

Query Match      51.8%; Score 44; DB 4; Length 847;
Best Local Similarity 46.7%; Pred. No. 51;
Matches 7; Conservative 1; Mismatches 7; Indels 7; Gaps 0;

Qy 1 HSSDYSMRKNQYVS 15
Db 230 HSSDYRFWESGELAS 244
|||||:|:|

RESULT 10
US-09-270-767-58735
; Sequence 58735, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58735
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-58735

Query Match      49.4%; Score 42; DB 4; Length 25;
Best Local Similarity 63.6%; Pred. No. 2.8;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HSSDYSMRKN 11
Db 5 HSSDYSMRKN 15
|||||:|:|

RESULT 11
US-09-248-796A-15562
; Sequence 15562, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 15562
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-15562
```

```
Query Match      49.4%; Score 42; DB 4; Length 250;
Best Local Similarity 40.0%; Pred. No. 31;
Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY      1 HSSDYSWMRKNOYV 15
      | | : : | | : | |
Db      209 HDSEFDLSRNTYIS 223

RESULT 12
US-09-072-917A-9
; Sequence 9, Application US/09072917A
; Patent No. 6288302
; GENERAL INFORMATION:
; APPLICANT: Yu, Su-May
; APPLICANT: Liu, Li-Fei
; APPLICANT: Chan, Ming-Tsair
; TITLE OF INVENTION: Application of Alpha-Amylase Gene
; TITLE OF INVENTION: Promoter and Signal Sequence in the Production of
; Patent No. 6288302
; TITLE OF INVENTION: Recombinant Proteins in Transgenic Plants and Transgenic
; TITLE OF INVENTION: Plant Seeds
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive/6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/072.917A
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/509,962
; FILING DATE: 01-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Gass, David A.
; REGISTRATION NUMBER: 38,153
; REFERENCE/DOCKET NUMBER: 28123/34257
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 435 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-072-917A-9

Query Match      49.4%; Score 42; DB 3; Length 435;
Best Local Similarity 60.0%; Pred. No. 54;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 HSSDYSWMRK 10
      | | | | |
Db      415 HGKDYSVWEK 424

RESULT 13
US-09-165-396-5
; Sequence 5, Application US/09165396
; Patent No. 641134
; GENERAL INFORMATION:
; APPLICANT: BECKER, JEFFREY W.
```

```
; APPLICANT: LUBKOWITZ, MARK A.
; TITLE OF INVENTION: ISOLATED CANDIDA ALBICANS OLIGOPEPTIDE TRANSPORTER GENE
; FILE REFERENCE: 372.6520P
; CURRENT APPLICATION NUMBER: US/09/165,396
; CURRENT FILING DATE: 1998-10-02
; EARLIER APPLICATION NUMBER: PCT/US98/02332
; EARLIER FILING DATE: 1998-02-06
; EARLIER APPLICATION NUMBER: 60/037,859
; EARLIER FILING DATE: 1997-02-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 877
; TYPE: PRT
; ORGANISM: S. cerevisiae
US-09-165-396-5

Query Match      49.4%; Score 42; DB 4; Length 877;
Best Local Similarity 42.9%; Pred. No. 1.1e+02;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      1 HSSDYSWMRKNOYV 14
      | | | | | : :
Db      36 HSSDPSQWYDEQI 49

RESULT 14
US-09-270-767-47885
; Sequence 47885, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47885
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-47885

Query Match      48.2%; Score 41; DB 4; Length 149;
Best Local Similarity 54.5%; Pred. No. 26;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      3 SDYSWMRKNOY 13
      | | | | | :
Db      125 SDYSVMQTKGY 135

RESULT 15
US-09-248-796A-25364
; Sequence 25364, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 25364
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Candida albicans
```


US-09-248-796A-25364

Query Match 48.2%; Score 41; DB 4; Length 297;
Best Local Similarity 50.0%; Pred. No. 53;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 4 DYSMWKKNQYVS 15
|||:|:|:|:|:|:
Db 270 DYSIWGNQLLA 281

Search completed: June 3, 2005, 08:31:27
Job time : 5.3625 secs

THIS PAGE BLANK (USPTO)